

60362

From: Zeman, Mary
Sent: Thursday, February 14, 2002 10:59 AM
To: STIC-Biotech/ChemLib
Subject: Interference search 09/636801

Please search SEQ ID NO: 392 of 09/636801 in pending files and US Patented files only. Paper printout please.

Thank you,
Mary K. Zeman
Examiner, 1631
305-7133
CM1 12A17
mailbox: CM1 12D01

CRFE

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 2/15/02
Date Completed: 2/15/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 02
WWW/Internet: _____
Other (specify): _____

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EXAMINER
WILLIAM P. SHERMAN
JULY 1964

Result No.	Score	Query Match	Length	DB	ID	Description
1	1574	100.0	309	6	US-10-010-742-209	Sequence 80, App1
2	1431	90.0	282	5	US-09-877-065-8	Sequence 9, App1
3	1431	90.9	282	5	US-09-889-723-291	Sequence 291, App1
4	1431	90.9	282	5	US-09-889-724-291	Sequence 291, App1
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7	1431	90.9	282	5	US-09-990-444-291	Sequence 291, App1
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45	1431	90.9	282	5	US-09-993-468-291	Sequence 291, App

ALIGNMENTS

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RESULT 1.
US-10-010-742-209
Sequence 209, Application US/10010742
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugui
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Wang, Tonglong
APPLICANT: McNeill, Patricia D.
APPLICANT: Harlocker, Susan L.
APPLICANT: Bennington, Angela Ann
APPLICANT: Zehentner, Barbara
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C7
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ. ID NOS: 307
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 209
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-010-742-209

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Best Local Similarity 100.0%; Pred. No. 1e-124;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps

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181 EVANDYNASSETLCEAPRMPPOPTVWVASVDGAFNSEVSNISFELNSEENTMKNVSV 240
QY 181 EVANDYNASSETLCEAPRMPPOPTVWVASVDGAFNSEVSNISFELNSEENTMKNVSV 240
Db 181 EVANDYNASSETLCEAPRMPPOPTVWVASVDGAFNSEVSNISFELNSEENTMKNVSV 240

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38	PRIOR FILING DATE: 1998-07-07
39	PRIOR APPLICATION NUMBER: 60/092182-01
40	PRIOR FILING DATE: 1998-07-09
41	PRIOR APPLICATION NUMBER: 60/092472-01

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Db	1	MASIQQLFMSIIITIIITIIILACAILIIIGFGISGHSHTVTTVVASAGIGEDGILSCFEE	60
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Db	61	DIKLSIDIYIOMLKEBVLGLVHEFKEGKDELSEODEMERGRATVAPADQIVIGNASLRUKV	120
Qy	148	QLTAGTGYKCYIITISKGGANLETKGAFSPMEPVNDVYNASSTLCEAPRMPPOPTVY	207
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Db	181	MASQVDQGANFSEVNSFELSENSEVNMKVVSVLVNTYINNVTSCMIENDIAKATGDIKV	240
Qy	268	TESETIKRSHIQLNLSKASLCVSSFPALISWMLPLPLSPYLMUK	309
Db	241	TESETIKRSHIQLNLSKASLCVSSFPALISWMLPLPLSPYLMUK	282

RESULT 4
US-09-989-724-291
; Sequence 291, Application US/09989724;
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavir, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC67
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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Query Match	90.9%;	Score 1431;	DB 5;	Length 282;
Best Local Similarity	100.0%;	Pred. No. 9.5e-113;		
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Db	1	MASLQQLFWMSIIIIIIILAGAIALIIIGFSGISGRHSITVTVVASAGNIGEDDILSTCFEP	60	
QY	88	DIKLSDIYIOWLKEGYVLGVHEFKKGKDBLSQODEMFRGRTAVFADQYIVGNASLRLKNV	147	
Db	61	DIKLSDIYIOWLKEGYVLGVHEFKKGKDBLSQODEMFRGRTAVFADQYIVGNASLRLKNV	120	
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Db      241  TSEIKRRSHQLNLSKRSKSLCVSFFPAISWALLPLPSYLMWK 282

RESULT      5
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: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Bolstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Guney, Austin L.
: APPLICANT: Kijavini, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tunas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C69
: CURRENT APPLICATION NUMBER: us/09/989,730
: CURRENT FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/088217
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;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088734
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 90.98; Score 1431; DB 5; Length 282;
Best Local Similarity 100.08; Pred. No. 9.5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLQILFWSIIITIIILACALIIIFGSIISGRSITVTIVASAGNIGEDGIIISCTREP 87
Db 1 MASLQILFWSIIITIIILACALIIIFGSIISGRSITVTIVASAGNIGEDGIIISCTREP 60
QY 88 DIKLSIDIVQWLKEGVGLVHEFKEGKDELSEODEMFGRGTAVFADQYIVGNASIRLKNV 147
Db 61 DIKLSIDIVQWLKEGVGLVHEFKEGKDELSEODEMFGRGTAVFADQYIVGNASIRLKNV 120
QY 148 QLTDAITKCYIITISKGNANLEKIGAFSMEPVYNDVYNASSETLRCEADRPWPPQTVV 207

|||||
Db 121 QLTAGTYKCYITISKSGKNANLEKGTAFSMPEVNVVDYNNASSETLRCEADPMFPQPIVV 180
Qy 208 WASOVDOANFSEVSNSEFEINSENVTKKVSVLNTNTNTSCMIENDIAKAGDIXV 267
Db 181 WASOVDOANFSEVSNSEFEINSENVTKKVSVLNTNTNTSCMIENDIAKAGDIXV 240
Qy 268 TESEIKRSHQLNLSKASLCVSSFFAISMLPLSPYLMK 309
Db 241 TESEIKRSHQLNLSKASLCVSSFFAISMLPLSPYLMK 282
RESULT 6
US-09-990-436-291
Sequence 291, Application US/09990436
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secitected and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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;; PRIOR FILING DATE: 1998-06-19
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQILFWSIIIIIIIIAGATAIIITGFIGSHSTIVTVTVASAGNIGEDGILSCFEP 87
DB 1 MASIGQILFWSIIIIIIIIAGATAIIITGFIGSHSTIVTVTVASAGNIGEDGILSCFEP 60
QY 88 DIKLSDIVIOMLKEGVGLVHEFEKEGDESEDEMRGRTAFAADOVIGNLSRLKNV 147
DB 61 DIKLSDIVIOMLKEGVGLVHEFEKEGDESEDEMRGRTAFAADOVIGNLSRLKNV 120
QY 148 QLTIDAGTYKCYIITTSKRGANLEKYTGAFSMEPVNDVNASSETLRCAPRMPPTVV 207
DB 121 QLTIDAGTYKCYIITTSKRGANLEKYTGAFSMEPVNDVNASSETLRCAPRMPPTVV 180
QY 208 MASOVQGANFSEVSNTSEFLNSENVTMKVSVLYNTINNTYSCHIENDIAATGDIK 267
DB 181 MASOVQGANFSEVSNTSEFLNSENVTMKVSVLYNTINNTYSCHIENDIAATGDIK 240
QY 268 TESEIKRSHLOLNSKASLCVSSFFAISWALLPSYMLK 309
DB 241 TESEIKRSHLOLNSKASLCVSSFFAISWALLPSYMLK 282

RESULT 7
US-09-990-444-291
; Sequence 291, Application US/09990444
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC19
; CURRENT APPLICATION NUMBER: US/09/990,444
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106

[illegible]

;; PRIOR FILING DATE: 1998-06-17
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;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01

;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472
Query Match 90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9, 5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 28 MASIGQILFWSTISITIIILAGAILIGFGISGRHSITVTVYASAGNIGEDGILSCTEP 87
Db 1 MASIGQILFWSTISITIIILAGAILIGFGISGRHSITVTVYASAGNIGEDGILSCTEP 60
Qy 88 DIKLSDIYIOWLKEGVGLVHEFEKGDLESEODEMFRGRTAVFADQYIVGNASRLKNV 147
Db 61 DIKLSDIYIOWLKEGVGLVHEFEKGDLESEODEMFRGRTAVFADQYIVGNASRLKNV 120
Qy 148 QLTDAGYTKCYIITISKGGANLEKTKGAFSPKEVNVNDYNASSETLRCBAPRPFQPIVY 207
Db 121 QLTDAGYTKCYIITISKGGANLEKTKGAFSPKEVNVNDYNASSETLRCBAPRPFQPIVY 180
Qy 208 WASQVDGAFNSEVNTSEFELNSENVTMKVSVLVNTVNTNNYSGMINDIAKATGDIKV 267
Db 181 WASQVDGAFNSEVNTSEFELNSENVTMKVSVLVNTVNTNNYSGMINDIAKATGDIKV 240
Qy 268 TESEIKRRSHQLNSKASLCVSSFFAISMALLPLSPYLMUK 309
Db 241 TESEIKRRSHQLNSKASLCVSSFFAISMALLPLSPYLMUK 282
RESULT 9
US-09-989-722-291
; Sequence 291, Application US/09989722
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paonl, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787

;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
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;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 MASIGQLIFWIIITITITLACALALITGFGISGRHSITVTTVASAGNIGEGCIIISCTPEP 87
Db 1 MASIGQLIFWIIITITITLACALALITGFGISGRHSITVTTVASAGNIGEGCIIISCTPEP 60
Qy 88 DIKLSDIYIOMLKEGVLCGLVHEFEKGEKDELSEODEMFGRTAVFADQYIVNASLRILNV 147
Db 61 DIKLSDIYIOMLKEGVLCGLVHEFEKGEKDELSEODEMFGRTAVFADQYIVNASLRILNV 120
Qy 148 QLTDAGYTKCYIITSKGNANLEYKYGAFSMEPEYNDVYNASSETLRCEAPRWFQPTIV 207
Db 121 QLTDAGYTKCYIITSKGNANLEYKYGAFSMEPEYNDVYNASSETLRCEAPRWFQPTIV 180
Qy 208 WASQVDOGANSFVSNFSFELNSENVTMKVSVLYNVTINNTYSMIENDIAKATGDIKY 267
Db 181 WASQVDOGANSFVSNFSFELNSENVTMKVSVLYNVTINNTYSMIENDIAKATGDIKY 240
Qy 268 TESEIKRSHQLNLSKASLCVSSFPFAISWALLPLSPYLMK 309
Db 241 TESEIKRSHQLNLSKASLCVSSFPFAISWALLPLSPYLMK 282

RESULT 10
US-09-989-725-291
;; Sequence 291, Application US/09989725
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerlitsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.

;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C71
;; CURRENT FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088030
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088734
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088742
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826

PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089600
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
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 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
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 PRIOR FILING DATE: 1998-06-18
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 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090246
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 PRIOR APPLICATION NUMBER: 60/090252
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 PRIOR APPLICATION NUMBER: 60/090254
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 PRIOR APPLICATION NUMBER: 60/090349
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 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
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 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090535
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
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 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090678
 PRIOR FILING DATE: 1998-06-25

PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090694
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
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 PRIOR APPLICATION NUMBER: 60/090862
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 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09
 PRIOR APPLICATION NUMBER: 60/092472

Query Match 90.9%; Score 1431; DB 5; Length 282;
 Best Local Similarity 100.0%; Pred. No. 9.5e-113;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGGILFWSTISIIIIAGAILIGISGRHSITVTVVASAGNIEDGILSTFEP 87
 DB 1 MASLGGILFWSTISIIIIAGAILIGISGRHSITVTVVASAGNIEDGILSTFEP 60
 QY 88 DIKLSDIVIQLWKEGVLGLVHEFEKSKDELSEDEDFRGRFVAFADQVTVGNASRLKRV 147
 DB 61 DIKLSDIVIQLWKEGVLGLVHEFEKSKDELSEDEDFRGRFVAFADQVTVGNASRLKRV 120
 QY 148 QLTDACTYCYIITSKGNANLEKYGAFSPMEVDVYNASSETLRCEAPRFPQPTVV 207
 DB 121 QLTDACTYCYIITSKGNANLEKYGAFSPMEVDVYNASSETLRCEAPRFPQPTVV 180
 QY 208 MASOVDOGANFSEVSWTSELSSENVTMKVSVLYVNTINNTYSCHIENDIAKATGDIV 267
 DB 181 MASOVDOGANFSEVSWTSELSSENVTMKVSVLYVNTINNTYSCHIENDIAKATGDIV 240
 QY 268 TESEIKRRSHLOLINSKASLCVSPFAISMAILPLSPYLMK 309
 DB 241 TESEIKRRSHLOLINSKASLCVSPFAISMAILPLSPYLMK 282

RESULT 11
 US-09-989-726-291
 Sequence 291, Application US/09989726
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Getzler, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Kijavira, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C60
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065166
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
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PRIOR APPLICATION NUMBER: 60/088030
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PRIOR APPLICATION NUMBER: 60/088033
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PRIOR APPLICATION NUMBER: 60/088326
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PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
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PRIOR APPLICATION NUMBER: 60/088217
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PRIOR APPLICATION NUMBER: 60/088555
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PRIOR APPLICATION NUMBER: 60/088810
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PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
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PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
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PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540

Query Match 90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.5e-113; Mismatches 0; Indels 0; Gaps 0;
Matches 282; Conservative 0;

QY 28 MASLQILFWMSITIIIIAGAILIIGFISGRHSITVTYVASAGNIGEDGILSTCFEP 87
DB 1 MASLQILFWMSITIIIIAGAILIIGFISGRHSITVTYVASAGNIGEDGILSTCFEP 60

QY 88 DIKLSIDIVOMKEGYLGIVHEFKESKDELSEODEMFRRTAVFADQVIVGNASLRLKNV 147
DB 61 DIKLSIDIVOMKEGYLGIVHEFKESKDELSEODEMFRRTAVFADQVIVGNASLRLKNV 120

QY 148 QLTDAQTYCYIITISGKGNANLEKKTGAFSMEPVVDYNASSETLRCEAPRMEPOPVTYV 207
DB 121 QLTDAQTYCYIITISGKGNANLEKKTGAFSMEPVVDYNASSETLRCEAPRMEPOPVTYV 180

QY 208 WASQVDQGANFSEVNTSELSSENVYTMKVSVLYNVNTINTNTYSCHIENDIAKATGDIVK 267
DB 181 WASQVDQGANFSEVNTSELSSENVYTMKVSVLYNVNTINTNTYSCHIENDIAKATGDIVK 240

QY 268 TESEIKRSHLOLLNSKASLCVSSFFAISMALLPLSPYIMLK 309
DB 241 TESEIKRSHLOLLNSKASLCVSSFFAISMALLPLSPYIMLK 282

RESULT 12
US-09-989-727-291
; Sequence 291, Application US/09989727
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferreira, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjaer, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC65
CURRENT FILING DATE: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202

RESULT 13
US-09-989-728-291
Sequence 291, Application US/09989728
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C72
CURRENT APPLICATION NUMBER: US/09/989,728
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 90.9%; Score 1431; DB 5; Length 282;

Best Local Similarity 100.0%; Pred. No. 9.5e-113; Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 MASIGQLFWIISIIIIIIAGAILIIFGIGSGRHSITVTTVASAGNIGEGGIIISCTPEP 87
Db 1 MASIGQLFWIISIIIIIIAGAILIIFGIGSGRHSITVTTVASAGNIGEGGIIISCTPEP 60
Qy 88 DIKLSDIVIOWLKEGVGLVHEFEKGEKDELSEODEMFRGPAVADVOYIVNASLRLKNV 147
Db 61 DIKLSDIVIOWLKEGVGLVHEFEKGEKDELSEODEMFRGPAVADVOYIVNASLRLKNV 120
Qy 148 QLTADAGTYKCYIITSKGNANLEKYGAFSMPENVNDVYNASSETLRCEAPRWFPOPTIV 207

Db 121 QLTADAGTYKCYIITSKGNANLEKYGAFSMPENVNDVYNASSETLRCEAPRWFPOPTIV 180
Qy 208 WASOYDGCANFSEVSNTEFELNSEVNTMKVSVLYNTNNTYSCMIENDIAKATGDIKV 267
Db 181 WASOYDGCANFSEVSNTEFELNSEVNTMKVSVLYNTNNTYSCMIENDIAKATGDIKV 240
Qy 268 TESEIKRRSHQLNLSKASLCVSSFFAISWALLPLSPYLMK 309
Db 241 TESEIKRRSHQLNLSKASLCVSSFFAISWALLPLSPYLMK 282

RESULT 14

US-09-989-731-291
Sequence 291, Application US/09989731

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Bolstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Poly peptides and Nucleic
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;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match          90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 MASLGGIIFWSSIIIIIIILAGALALIIGFGISGRSITVTVTVASAGNIGEDGILSCTEEP 87
        |||||
Db       1 MASLGQIIFWSSIIIIIIIILAGALALIIGFGISGRSITVTVTVASAGNIGEDGILSCTEEP 60
        |||||

QY      88 DIKLSDIYIQWLKEGVGLTVEHFEKGEKDELSEODMEFGRPAVFADQIVGNASRLKNV 147
        |||||
Db       61 DIKLSDIYIQWLKEGVGLTVEHFEKGEKDELSEODMEFGRPAVFADQIVGNASRLKNV 120
        |||||

QY      148 QLTDAGYKYCYIITSKGNGANLEKYTGCAFSPENVNDYNASSELRCEAPRMFPQPIVV 207
        |||||
Db       121 QLTDAGYKYCYIITSKGNGANLEKYTGCAFSPENVNDYNASSELRCEAPRMFPQPIVV 180
        |||||

QY      208 WASOVDOGANSFYNSNTSFELENSEVTMKVVSYLEYNTINNTYSCEMIENDIAKATGDIV 267
        |||||
Db       181 WASOVDOGANSFYNSNTSFELENSEVTMKVVSYLEYNTINNTYSCEMIENDIAKATGDIV 240
        |||||

QY      268 TSESIKRSHQLNLNSKASCLVSSPFAISMALLPLSPYLMLK 309
        |||||
Db       241 TSESIKRSHQLNLNSKASCLVSSPFAISMALLPLSPYLMLK 282

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Search completed: February 15, 2002, 14:22:46
Job time: 196 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 15, 2002, 14:18:55 : Search time 12.65 Seconds

(without alignments)
549.685 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574
Sequence: 1 HASAHASGRQLHSASTQI.....SSFPAISWALPLSPYLMK 309

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PTUTS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217.5	13.8	540	2	US-08-724-394A-4
2	212.5	13.5	610	2	US-08-724-394A-5
3	211.5	13.4	589	2	US-08-724-394A-1
4	207.5	13.2	342	2	US-08-724-394A-6
5	186	11.8	581	2	US-08-724-394A-2
6	183	11.6	581	2	US-08-724-394A-3
7	147.5	9.4	323	5	PCT-US94-09642-2
8	147.5	9.4	329	2	US-08-456-104-2
9	147.5	9.4	329	2	US-08-101-624-2
10	147.5	9.4	329	3	US-08-479-744A-2
11	147.5	9.4	329	4	US-08-280-757B-2
12	147.5	9.4	329	4	US-08-205-697A-23
13	147.5	9.4	329	4	US-08-702-525-23
14	147.5	9.4	329	5	PCT-US95-02576-23
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16	143.5	9.1	309	2	US-08-456-104-4
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21	143.5	9.1	309	5	PCT-US95-02576-21
22	143.5	9.1	314	4	US-08-205-697A-13
23	143.5	9.1	314	4	US-08-702-525-13
24	143.5	9.1	314	5	PCT-US95-02576-13
25	132	8.4	860	5	PCT-US95-08493-15
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28	132	8.4	868	2	US-08-644-271-1	Sequence 1, Appl
29	132	8.4	868	5	PCT-US95-08493-21	Sequence 21, Appl
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31	128	8.1	365	4	US-08-928-383B-24	Sequence 24, Appl
32	127	8.1	946	5	PCT-US95-08493-13	Sequence 15, Appl
33	124.5	7.9	208	3	US-08-630-172-15	Sequence 15, Appl
34	124.5	7.9	208	4	US-08-375-419-15	Sequence 15, Appl
35	124	7.9	306	2	US-08-147-772-4	Sequence 4, Appl
36	124	7.9	306	2	US-08-456-104-8	Sequence 8, Appl
37	124	7.9	306	2	US-08-101-624-25	Sequence 25, Appl
38	124	7.9	306	3	US-08-153-262-4	Sequence 4, Appl
39	124	7.9	306	3	US-08-479-744A-31	Sequence 31, Appl
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41	124	7.9	306	4	US-09-159-135-4	Sequence 4, Appl
42	124	7.9	306	4	US-08-205-697A-17	Sequence 17, Appl
43	124	7.9	306	4	US-08-702-525-17	Sequence 17, Appl
44	124	7.9	306	5	PCT-US95-02576-17	Sequence 17, Appl
45	124	7.9	320	4	US-08-205-697A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-724-394A-4
: Sequence 4, Application US/08724394A
: Patent No. 5872237
: GENERAL INFORMATION:
: APPLICANT: Feder, John N.
: APPLICANT: Kronmal, Gregory S.
: APPLICANT: Lauer, Peter M.
: APPLICANT: Ruddy, David A.
: APPLICANT: Thomas, Winston
: APPLICANT: Tsuchihashi, Zenta
: APPLICANT: Wolf, Roger K.
: TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
: TITLE OF INVENTION: Sequences and Antibodies Thereeto
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
: STREET: Two Embarcadero Center, 8th floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/724,394A
: FILING DATE: 01-OCT-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitts, Renee A. 35,136
: REGISTRATION NUMBER: 017957-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-576-0200
: TELEFAX: 415-576-0300
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 540 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..540
: OTHER INFORMATION: /note= "BIFS"
US-08-724-394A-4

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Query Match Score 13.8%; Score 217.5; DB 2; Length 540:
Best Local Similarity 25.6%; Pred. No. 7.3e-14;
Matches 56; Conservative 45; Mismatches 10; Indels 17; Gaps 7;

QY 62 HSIYTVASAGNI---GEDGIISCTEPPDIKLSDIYIOWLKEGVLGVHFEKGEKDEL 117
Db 30 HSAQPSVSLGSPGPIIAMVGEDADLCCHLFPPTSAETMELKVVSSSIQRYVNVYADGKEVE 89
QY 118 SEQDFMFGRTVAFADQYIVGNASRLKKNVOLDIGTKCYITLTKGKNALFKTTGAF 177
Db 90 DROSAFPGYGRISILDLGDTAGKAALRIHVNTASDSGKYLCLFQDDDFEKAIVELKVAAL 149
QY 178 SKEPVNVD---YMASSETLRCEAPRMFPQPTVYMASQYDOGANFSEVSTSEELISENYT 234
Db 150 G-SDLHVYKVGKIDGCIHLCEKSTQWYQPOIQWNSN--NKGEN--IPVEAPVYADGVG 203
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1 RESULT 2
2 US-08-724-394A-5
3 : Sequence 5, Application US/08724394A
4 : Patent No. 5872237
5 :
6 : GENERAL INFORMATION:
7 : APPLICANT: Feder, John N.
8 : APPLICANT: Krommal, Gregory S.
9 : APPLICANT: Laufer, Peter M.
10 : APPLICANT: Ruddy, David A.
11 : APPLICANT: Thomas, Winston
12 : APPLICANT: Tsuchinashi, Zenta
13 : TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
14 : TITLE OF INVENTION: Sequences and Antibodies Thereco
15 : NUMBER OF SEQUENCES: 31
16 :
17 : CORRESPONDENCE ADDRESSES:
18 : ADDRESSEE: TOWNSEND and CREW LLP
19 : STREET: Two Embarcadero Center, 8th Floor
20 : CITY: San Francisco
21 : STATE: CA
22 : COUNTRY: USA
23 : ZIP: 94111-3834
24 :
25 : COMPUTER READABLE FORM:
26 : MEDIUM TYPE: Floppy disk
27 : COMPUTER: IBM PC compatible
28 : OPERATING SYSTEM: PC-DOS/MS-DOS
29 : SOFTWARE: PatentIn Release #1.0, Version #1.30
30 : CURRENT APPLICATION DATA:
31 : APPLICATION NUMBER: US/08/724,394A
32 : FILING DATE: 01-OCT-1996
33 : CLASSIFICATION: 536
34 : ATTORNEY/AGENT INFORMATION:
35 : NAME: Filts, Renee A.
36 : REGISTRATION NUMBER: 35,136
37 : REFERENCE/DOCKET NUMBER: 017957-000100
38 : TELECOMMUNICATION INFORMATION:
39 : TELEPHONE: 415-576-0300
40 : TELEFAX: 415-576-0300
41 : INFORMATION FOR SEQ ID NO: 5:
42 : SEQUENCE CHARACTERISTICS:
43 : LENGTH: 610 amino acids
44 : TYPE: amino acid
45 : STRANDEDNESS: not relevant
46 : TOPOLOGY: not relevant
47 : MOLECULE TYPE: peptide
48 : FEATURE:
49 : NAME/KEY: Region
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51 : OTHER INFORMATION: /note="BTF3"
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53 : US-08-724-394A-5

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[illegible]

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3      ; Sequence 1, Application US/08724394A
4      ; Patent No. 5872237
5      ;
6      GENERAL INFORMATION:
7      APPLICANT: Feder, John N.
8      APPLICANT: Kromal, Gregory S.
9      APPLICANT: Laufer, Peter M.
10     APPLICANT: Ruddy, David A.
11     APPLICANT: Thomas, Winston
12     APPLICANT: Tsuchihashi, Zenta
13     APPLICANT: Wolff, Roger K.
14     TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
15     TITLE OF INVENTION: Sequences and Antibodies Thereco
16     NUMBER OF SEQUENCES: 31
17     CORRESPONDENCE ADDRESSES:
18     ADDRESSEE: TOWNSEND and CREW LLP
19     STREET: Two Embarcadero Center, 8th Floor
20     CITY: San Francisco
21     STATE: CA
22     COUNTRY: USA
23     ZIP: 94111-3834
24     COMPUTER READABLE FORM:
25     MEDIUM TYPE: Floppy disk
26     COMPUTER: IBM PC compatible
27     OPERATING SYSTEM: PC-DOS/MS-DOS
28     SOFTWARE: Patent In Release #1.0, Version #1.30
29     CURRENT APPLICATION DATA:
30     APPLICATION NUMBER: US/08/724,394A
31     FILING DATE: 01-OCT-1996
32     CLASSIFICATION: 536
33     ATTORNEY/AGENT INFORMATION:
34     NAME: Filts, Renee A.
35     REGISTRATION NUMBER: 35,136
36     REFERENCE/DOCKET NUMBER: 017957-000100
37     TELECOMMUNICATION INFORMATION:
38     TELEPHONE: 415-576-0200
39     TELEFAX: 415-576-0300
40     INFORMATION FOR SEQ ID NO: 1:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 589 amino acids
43     TYPE: amino acid
44     STRANDEDNESS: not relevant
45     TOPOLOGY: not relevant
46     MOLECULE TYPE: peptide
47     FEATURE:
48     NAME/KEY: Region
49     LOCATION: 1..589
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Query Match          13.4%; Score 211.5; DB 2; Length 589;
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 Db 222 YION 225

RESULT 4
 ; Sequence 6, Application US/08724394A
 ; Patent No. 5872237
 ; GENERAL INFORMATION:
 ; APPLICANT: Feder, John N.
 ; APPLICANT: Kronmal, Gregory S.
 ; APPLICANT: Laufer, Peter M.
 ; APPLICANT: Ruddy, David A.
 ; APPLICANT: Thomas, Winston
 ; APPLICANT: Tsuchihashi, Zenta
 ; APPLICANT: Wolff, Roger K.
 ; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
 ; TITLE OF INVENTION: Sequences and Antibodies Thereto
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 ; STREET: Two Embarcadero Center, 8th floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/724,394A
 ; FILING DATE: 01-Oct-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Flits, Renee A.
 ; REGISTRATION NUMBER: 35,136
 ; REFERENCE/DOCKET NUMBER: 017957-000100
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-576-0200
 ; TELEFAX: 415-576-0200
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 342 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Region
 ; LOCATION: 1..342
 ; OTHER INFORMATION: /note= "BTF4"
 ;
 ; US-08-724-394A-6

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Query Match      13.2%; Score 207.5; DB 2; Length 342;
Best Local Similarity 26.1%; Pred. No. 3.7e-13;
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

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   :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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QY 241 LYNTVINTNTYSCMIENDI-AKATGDIKYTE 269
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RESULT 5
US-08-724-394A-2
Sequence 2, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..581
OTHER INFORMATION: /note= "BFP1"
US-08-724-394A-2

```

Query Match 11.8%; Score 186; DB 2; Length 581;
 Best Local Similarity 23.6%; Pred. No. 1.4e-10;
 Matches 52; Conservative 41; Mismatches 115; Indels 12; Gaps 5;

QY 42 IITLLGAVLILGFGSGRHSITVTVASAGNIGEDGLSCFFEPDIKSDIVIQMLK 101
 Db 19 LLLLLSLCAL-----VSAQFIVGPDPLATVGEHTTIRCHLSPKNAEDMEVWFRS 73
 QY 102 GVLGVHEFEKGDDELSEODEMFRGTAVFADQIVGNASLRKNVQLTDACTYKCIIT 161
 Db 74 QFSPAVFYVYKGRRETEQMEYRGRTTFVSKISRGVALYHNITAQENGIRCFQ 133
 QY 162 SKKGNANLE-YKTGAFSMEPVNV-DYNASSELRCEAPRWPQPTVYVASQVDGA-NF 218
 Db 134 GRSDYDAILHLVYVAGLSKPLISMGRGHEDGIRLECISRGWYKPLTWMDPYGVAPAL 193
 QY 219 SEVSNTSFELSENVTMKVSVLYNTVINTYSCMIENDI 258
 Db 194 KEYSMP---DADGLFMVTTAVIIRDKSVRNMSCSINNTL 229

RESULT 6

US-08-724-394A-3

Sequence 3, Application US/08724394A

Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Kronmal, Gregory S.

APPLICANT: Lauer, Peter M.

APPLICANT: Ruddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

NUMBER OF SEQUENCES: 31

TITLE OF INVENTION: Sequences and Antibodies thereto

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 01/957-000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 581 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: 1..581

OTHER INFORMATION: /note- "BTF2"

US-08-724-394A-3

Query Match 11.6%; Score 183; DB 2; Length 581;
 Best Local Similarity 23.6%; Pred. No. 2.9e-10;
 Matches 59; Conservative 42; Mismatches 113; Indels 36; Gaps 8;

QY 23 EEPSPM-----ASLGQILFMSITSIITIIAGALALLIGFISGRHSITVTVASAGNI-- 75
 Db 2 EPAALHFSLPASL-----LLLLLLLSLICALV-----SAQFVYVAPAPITLA 45
 QY 76 -GEDGLSCFFEPDIKSDIVIQMLKEGVLGVHEFEKGDDELSEODEMFRGTAVFAD 133
 Db 46 MGEENTTLRCHLSPKNAEDMEVWFRSQSPSPAVFYVYKGRRETEQMEYRGRTTFVSK 105
 QY 134 QVTVGNASLRKNVQLTDACTYKCIITTSKGNANLE-YKTGAFSMEPVNV-DYNASSE 191
 Db 106 DINRGSAVALYHNITAQENGIRCFQEGRSYDEAILRLVYVAGLSKPLIEIKAQEDGS 165
 QY 192 TLRCAPRWPQPTVYVASQVDGANFSEVSNTSFEL---NSENVTKVSVLYNTVIN 248
 Db 166 WLECSIGGWYPEPLTWMDP-----YGEVVPALKEVSIADADGLFMVTTAVIIRDKYVR 219
 QY 249 TYSQMIENDI 258
 Db 220 NVSCSVNNTL 229

RESULT 7

PCT-US94-09642-2

Sequence 2, Application PC/TUS9409642

GENERAL INFORMATION:

APPLICANT: Purified Mammalian CTLA-4 Binding

TITLE OF INVENTION: Protein and Related Reagents

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schering-Plough Corporation, M-3-W

STREET: One Giralda Farms

CITY: Madison

STATE: New Jersey

COUNTRY: USA

ZIP: 07940-1000

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh IIcx

OPERATING SYSTEM: System Software 7.1

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/09642

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/120,606

FILING DATE: 13-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/116,882

FILING DATE: 03-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Blasdale, John H. C.

REGISTRATION NUMBER: 31,895

REFERENCE/DOCKET NUMBER: DX0390K1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-822-7039

TELEFAX: 201-822-7398

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 323 amino acids

TYPE: amino acid

TOPOLOGY: 1linear

MOLECULE TYPE: protein

PCT-US94-09642-2

Query Match 9.48; Score 147.5; DB 2; Length 329;

Query Match	9.4%;	Score 147.5;	DB 2;	Length 329;
Best Local Similarity	23.4%;	Pred. No. 5.3e-07;		
Matches 67;	Conservative 43;	Mismatches 109;	Indels 67;	Gaps 13

MOLECULE TYPE: protein
US-08-280-757B-2

Query Match 9.4%; Score 147.5; DB 4; Length 329;
Best Local Similarity 23.4%; Pred. No. 5.3e-07;
Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;

QY 50 IALLIGFSGRHSITVTTVASAGNIGEDGILCTF--EPDIKLSDIYQWLKEGVGLV 107
DB 12 ILFWAFLSCAAPLIKAY-----FNETADLPQFANSQNSLSLWFMODQENL-VL 65
QY 108 HEFKGKDELSDQDEMPGRTAVFADQYIVGNASRLKNVOLTDACTKCYITTSKGG- 166
DB 66 NEVYLKKEKPDVSHSKYMGRTSFDSD-----SWTLRLNLQIKDKGLQCIHKKPTGM 120
QY 167 -----NANLEYKTGA-FSMPEV---NDVYNASSETLRCEAPRMFPQPVVWASQVDOGAN 217
DB 121 IRIHQMSLSVLANFSQPEIYIPISNITENYVI-NLTCSSIHGYEP----- 166
QY 218 FSEVNTSEFELSENVTMKV-----VSVLNVTI-----NNTYSCMIEN 256
DB 167 ----KKMSVLLTKTKNSTLEYDGIQKSDQNVTELDVDSISLSVSPDVTSMNTICILET 222
QY 257 DIAKATGDIKYESEIKR--RSHLOLNS---KASLCVSPFAISM 297
DB 223 DKTRLSSPFSIELEDPPQPDHPIWITAVLPTVIICVWFCLILM 268

RESULT 12
US-08-205-697A-23
Sequence 23, Application US/08205697A
Patent No. 6218510
GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-205-697A-23

Query Match 9.4%; Score 147.5; DB 4; Length 329;

Best Local Similarity 23.4%; Pred. No. 5.3e-07;
Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;

QY 50 IALLIGFSGRHSITVTTVASAGNIGEDGILCTF--EPDIKLSDIYQWLKEGVGLV 107
DB 12 ILFWAFLSCAAPLIKAY-----FNETADLPQFANSQNSLSLWFMODQENL-VL 65
QY 108 HEFKGKDELSDQDEMPGRTAVFADQYIVGNASRLKNVOLTDACTKCYITTSKGG- 166
DB 66 NEVYLKKEKPDVSHSKYMGRTSFDSD-----SWTLRLNLQIKDKGLQCIHKKPTGM 120
QY 167 -----NANLEYKTGA-FSMPEV---NDVYNASSETLRCEAPRMFPQPVVWASQVDOGAN 217
DB 121 IRIHQMSLSVLANFSQPEIYIPISNITENYVI-NLTCSSIHGYEP----- 166
QY 218 FSEVNTSEFELSENVTMKV-----VSVLNVTI-----NNTYSCMIEN 256
DB 167 ----KKMSVLLTKTKNSTLEYDGIQKSDQNVTELDVDSISLSVSPDVTSMNTICILET 222
QY 257 DIAKATGDIKYESEIKR--RSHLOLNS---KASLCVSPFAISM 297
DB 223 DKTRLSSPFSIELEDPPQPDHPIWITAVLPTVIICVWFCLILM 268

RESULT 13
US-08-702-525-23
Sequence 23, Application US/08702525
Patent No. 6294660
GENERAL INFORMATION:
APPLICANT: Sharpe, Sharpe
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon
APPLICANT: Nadler, Lee
TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
TITLE OF INVENTION: Molecules and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,525
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-525-23

Query Match 9.4%; Score 147.5; DB 4; Length 329;
Best Local Similarity 23.4%; Pred. No. 5.3e-07;
Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;

Fri Feb 15 14:25:08 2002

us-09-636-801-392.ra1

Page 9

Db 49 VELPCRISPGKNATGMEGVWRPFESRVVHLIRNGKQDDQAPERYGRFELLKDAIGES 108

Qy 139 NASLRKLVQLTLDGATKCYITTSKGGANLETKTGAFSMEPVNDYNNASSETLCEAP 198

Db 109 KVTLRIRNRVRSDEGGTCEFRHDSYDEEAME-----LKEVDP 147

Qy 199 RMFQPTVYVMAISQVDOGANSEVSANTSFEIENSRVPMKRVSY-LYNYTINNTSCM 253

Db 148 FYWVSPGL-----VLAVLPVLLQITTVGLVFLCL 178

Search completed: February 15, 2002, 14:19:48
Job time: 53 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2002, 14:18:55 ; Search time 23.56 Seconds
(without alignments)
971.505 Million cell updates/sec

Title: US-09-636-801-392
Perfect score: 1574
Sequence: 1 HASAHASGRQQLHSASTQI.....SSFAISWALLPLSPYMLK 309

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1574	100.0	309	21	AA12556
2	1574	100.0	309	22	AA12556
3	1431	90.9	282	21	AA12557
4	1431	90.9	282	21	AA12557
5	1431	90.9	282	22	AA12557
6	1431	90.9	282	22	AA12557
7	1431	90.9	282	22	AA12557
8	842.5	53.5	195	22	AA12557
9	301	19.1	63	22	AA12557
10	246	15.6	387	22	AA12557
11	246	15.6	441	22	AA12557

12	246	15.6	534	22	AA00906	Human B lymphocyte
13	246	15.6	534	22	AA00906	Human membrane or
14	246	15.6	534	22	AA00906	Human amyloid prec
15	246	15.6	1020	22	AA00906	Human polypeptide
16	245	15.6	340	22	AA00906	Human B lymphocyte
17	241	15.3	316	20	AA00906	Human PRO352 prote
18	241	15.3	316	21	AA00906	Human PRO352 (UNO3
19	239	15.2	244	22	AA00906	Human B7-H3 polype
20	239	15.2	316	22	AA00906	Human B7-H3 polype
21	239	15.2	316	22	AA00906	Human gene 2 encod
22	239	15.2	534	22	AA00906	Human amyloid prec
23	237	15.1	216	22	AA00906	Human polypeptide
24	232.5	14.8	216	22	AA00906	Human B7-H3 polype
25	232.5	14.8	216	22	AA00906	Human gene 2 encod
26	225.5	14.3	466	21	AA00906	Human PRO1472 (UNO
27	225.5	14.3	466	22	AA00906	Human membrane ass
28	225.5	14.3	466	22	AA00906	Human PRO1472. Ho
29	225.5	14.3	466	22	AA00906	Protein of the inv
30	225	14.3	337	22	AA00906	Gene #1 associated
31	225	14.3	349	22	AA00906	Secreted protein e
32	225	14.3	414	22	AA00906	Protein encoded by
33	224.5	14.3	461	21	AA00906	Bovine butyrophill
34	223	14.2	513	19	AA00906	Human secreted pro
35	222.5	14.1	461	21	AA00906	Human PRO1347 (UNO
36	222.5	14.1	500	21	AA00906	Human PRO1347. Ho
37	222.5	14.1	500	22	AA00906	Protein of the inv
38	222.5	14.1	500	22	AA00906	Gene 47 related pe
39	219.5	13.9	513	22	AA00906	Bovine butyrophill
40	219.5	13.9	526	20	AA00906	BBIR II protein en
41	218	13.9	319	21	AA00906	Bovine butyrophill
42	213.5	13.6	584	19	AA00906	Human butyrophill
43	211.5	13.4	526	20	AA00906	Human myelin oligo
44	209	13.3	223	19	AA00906	Human butyrophill
45	207.5	13.2	319	19	AA00906	Bovine butyrophill

ALIGNMENTS

RESULT 1	AA12556	standard; Protein: 309 AA.
ID	AA12556	
AC	AA12556	
XX	AA12556	
XX	AA12556	
DT	07-NOV-2000	(first entry)
XX	07-NOV-2000	
DE	Human ovarian carcinoma antigen OBE protein SEQ ID NO:392.	
KW	Human: ovarian carcinoma; ovarian cancer; therapy; diagnosis;	
KW	tumour antigen; identification; cytostatic; gene therapy; vaccine.	
XX	Homo sapiens.	
OS	Homo sapiens.	
PN	WO200036107-A2.	
XX	22-JUN-2000.	
PD	22-JUN-2000.	
XX	22-JUN-2000.	
PF	17-DEC-1999;	99MO-US30270.
XX	17-DEC-1999;	99MO-US30270.
PR	17-DEC-1998;	98US-0215681.
PR	17-DEC-1998;	98US-0216003.
PR	23-JUN-1999;	99US-0338933.
PR	24-SEP-1999;	99US-0404879.
PA	(CORI-) CORIXA CORP.	
XX	(CORI-) CORIXA CORP.	
PI	Mitcham JL, King GE, Algate PA, Frudakis TN;	
XX	Mitcham JL, King GE, Algate PA, Frudakis TN;	
DR	WPI: 2000-431589/37.	
XX	WPI: 2000-431589/37.	
PT	Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of	

PT cancer, preferably ovarian cancer -
 XX
 PS Example 2; Page 205-206; 299pp; English.
 XX
 CC The present invention describes an isolated polypeptide comprising an
 CC immunogenic portion of an ovarian carcinoma protein (or its variants).
 CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
 CC cytostatic activity and can be used in gene therapy and vaccines.
 CC Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines
 CC are useful for the prevention, diagnosis and treatment of cancer.
 CC preferably ovarian cancer. AAB6951 to AAB7007 and AAB12552 to AAB12557
 CC represent human ovarian carcinoma polynucleotides and proteins used in
 CC the exemplification of the present invention.
 CC
 XX
 SQ Sequence 309 AA:
 Query Match 100.0%; Score 1574; DB 21; Length 309;
 Best Local Similarity 100.0%; Pred. No. 2.4e-131;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HASAHASGRQRLHSASTQIRWEPSPAMASLGQILFWSITSIITLLAGATALLTGFGISG 60
 DB 1 hasahasgrqlhsastqlrweppamaslqllfwsitsllllagatallltgfgisg 60
 QY RHSITVTVASAGNIGEDGILSCTFEPDRLSDIVIQWLKEGYLGLVHEFEKGDSEQ 120
 DB 61 rhsitvtvasagnigedgillsctfepdrlksdlvqlwkegylglvhefkegkdelseq 120
 QY 121 DEMFRGRTAVFAOVIVGNASRLKKNVQLTDAGTYCYITTSKGNANLEYTGAFSMP 180
 DB 121 demfrgrtavfadvivgnasrlknvqltdagtykyltskgnanleytgafsm 180
 QY 181 EVNVVDYNASSETLRCEAPRFPPQPTVYMASQVQGANFSEVNTSELSNENTMKVSV 240
 DB 181 evnvvdynasetlrceaprfppqptvyvasqvqganfsevnstsefelsenentmkvsv 240
 QY 241 LYNVTTNNNTYSCEIENDIAKATGDIKYTESEIKRRSHLOLNSKASLCVSPFAISWALL 300
 DB 241 lylvttntnyscmiendiakatgdikeyteiseikrrshlollnskaslcvsffaiswall 300
 -QY 301 PLSPYLMK 309
 DB 301 plspylmk 309
 RESULT 2
 AAB9205
 ID AAB9205 standard; Protein: 309 AA.
 XX
 AC AAB9205;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human ovarian tumour-derived antigen OBE #2.
 XX
 KW Cytostatic; human; breast tumour protein; breast cancer;
 KW ovarian tumour; antigen; OBE.
 XX
 OS Homo sapiens.
 XX
 PN WO200140269-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 29-NOV-2000; 2000WO-US32520.
 XX
 PR 30-NOV-1999; 99US-0451651.
 PR 22-FEB-2000; 2000US-0510662.
 PR 10-MAR-2000; 2000US-0523586.
 PR 07-APR-2000; 2000US-0545068.
 PR 15-MAY-2000; 2000US-0571025.
 XX

PA (CORI-) CORIXA CORP.
 XX
 PT Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
 XX
 DR WPI; 2001-356154/37.
 XX
 XX N-PADB; AAH55681.
 PT Breast tumor polypeptides and the nucleic acids that encode them,
 PT useful for the prevention, diagnosis and treatment of breast cancer -
 XX
 PS Example 3; Page 191-192; 221pp; English.
 CC
 CC The present invention relates to human breast tumour protein coding
 CC sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and
 CC AAH55682-AAH55762). The breast tumour protein DNA sequences may be used
 CC in the prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the breast tumour protein e.g. breast
 CC cancer. The present sequence is a human ovarian tumour-derived antigen,
 CC which was used in an example from the present invention.
 CC
 XX
 SQ Sequence 309 AA:
 Query Match 100.0%; Score 1574; DB 22; Length 309;
 Best Local Similarity 100.0%; Pred. No. 2.4e-131;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HASAHASGRQRLHSASTQIRWEPSPAMASLGQILFWSITSIITLLAGATALLTGFGISG 60
 DB 1 hasahasgrqlhsastqlrweppamaslqllfwsitsllllagatallltgfgisg 60
 QY RHSITVTVASAGNIGEDGILSCTFEPDRLSDIVIQWLKEGYLGLVHEFEKGDSEQ 120
 DB 61 rhsitvtvasagnigedgillsctfepdrlksdlvqlwkegylglvhefkegkdelseq 120
 QY 61 EVNVVDYNASSETLRCEAPRFPPQPTVYMASQVQGANFSEVNTSELSNENTMKVSV 240
 DB 61 evnvvdynasetlrceaprfppqptvyvasqvqganfsevnstsefelsenentmkvsv 240
 QY 121 DEMFRGRTAVFAOVIVGNASRLKKNVQLTDAGTYCYITTSKGNANLEYTGAFSMP 180
 DB 121 demfrgrtavfadvivgnasrlknvqltdagtykyltskgnanleytgafsm 180
 QY 181 EVNVVDYNASSETLRCEAPRFPPQPTVYMASQVQGANFSEVNTSELSNENTMKVSV 240
 DB 181 evnvvdynasetlrceaprfppqptvyvasqvqganfsevnstsefelsenentmkvsv 240
 QY 241 LYNVTTNNNTYSCEIENDIAKATGDIKYTESEIKRRSHLOLNSKASLCVSPFAISWALL 300
 DB 241 lylvttntnyscmiendiakatgdikeyteiseikrrshlollnskaslcvsffaiswall 300
 -QY 301 PLSPYLMK 309
 DB 301 plspylmk 309
 RESULT 3
 AAB12557
 ID AAB12557 standard; Protein: 282 AA.
 XX
 AC AAB12557;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human ovarian carcinoma antigen OBE protein SEQ ID NO:393.
 XX
 KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
 KW tumour antigen; identification; cytostatic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200036107-A2.
 XX
 PD 22-JUN-2000.
 XX
 PF 17-DEC-1999; 99WO-US30270.
 XX

PR 17-DEC-1998; 98US-0215681.
PR 17-DEC-1998; 98US-0216003.
PR 23-JUN-1999; 99US-0338933.
PR 24-SEP-1999; 99US-0404879.
XX
XX (CORI-) CORIXA CORP.
PI Mitcham JL, King GE, Algate PA, Frudakis TN;
XX WPI; 2000-431589/37.
XX
XX
XX Immunogenic portion of an ovarian carcinoma protein and the nucleic
PT acid encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer -
XX
XX
PS Example 2; Page 207; 299pp; English.
XX
XX The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants),
CC ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytotatic activity and can be used in gene therapy and vaccines.
CC Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines
CC are useful for the prevention, diagnosis and treatment of cancer,
CC preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557
CC represent human ovarian carcinoma polynucleotides and proteins used in
CC the exemplification of the present invention.
XX
XX
SO Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 21; Length 282;
Best Local Similarity 100.0%; Pred. No. 9, 6e-119;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQLFWISIIIIILAGALILIFGIGSRHSITVTVASAGNIGEDGILSCTEEP 87
DB 1 masigqllfwislllllagaalilifgfgsgrhsitvtvasagmldgdlscfep 60
QY 88 DIKSDIVIMLKGCVGLVHFEKGEDELSEODEMRGRRAVADQYIVNASLRILKNV 147
DB 61 diklsdvlwlgkvglvghfekgdelseodemrgravradvqivgnaslrilknv 120
QY 148 QLTADAGTYKCYIITSKSGKGNANLEYKTGAFSMPEVNVYNASSETLRCEARMPPOPTVY 207
DB 121 qltdagtykcyiltsksgkgnanleyktgafsmpevnyvynassettlrcearmpfpoptv 180
QY 208 WASQVDGAGNESEVSNTSFELNSENVTMKVSVLYNTTNTTSCMTENDIAKATGDIKV 267
DB 181 wasqvddganfsevsntsfelnseenvtmkvsvlynttnttscmtendiakatgdlkv 240
QY 268 TESFIKRRSHQLINSAKSLCVSFFAISWALLPLSPILMK 309
DB 241 tsefikrrshqlinsakslcvssffaiswallplspilmk 282

RESULT 4
AAY66719
ID AAY66719 standard; protein; 282 AA.
XX
XX AAY66719;
XX
XX 05-APR-2000 (first entry)
XX
XX Membrane-bound protein PRO1291.
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KM pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX Homo sapiens.
XX
XX WO963088-A2.
XX
XX PN
XX 09-DEC-1999.

XX
XX 02-JUN-1999; 99WO-US12252.
XX
XX 02-JUN-1998; 98US-0087607.
XX 02-JUN-1998; 98US-0087609.
XX 02-JUN-1998; 98US-0087759.
XX 03-JUN-1998; 98US-0087827.
XX 04-JUN-1998; 98US-0088021.
XX 04-JUN-1998; 98US-0088025.
XX 04-JUN-1998; 98US-0088028.
XX 04-JUN-1998; 98US-0088029.
XX 04-JUN-1998; 98US-0088030.
XX 04-JUN-1998; 98US-0088033.
XX 04-JUN-1998; 98US-0088136.
XX 05-JUN-1998; 98US-0088167.
XX 05-JUN-1998; 98US-0088202.
XX 05-JUN-1998; 98US-0088212.
XX 05-JUN-1998; 98US-0088217.
XX 09-JUN-1998; 98US-0088655.
XX 10-JUN-1998; 98US-0088722.
XX 10-JUN-1998; 98US-0088730.
XX 10-JUN-1998; 98US-0088734.
XX 10-JUN-1998; 98US-0088738.
XX 10-JUN-1998; 98US-0088740.
XX 10-JUN-1998; 98US-0088741.
XX 10-JUN-1998; 98US-0088742.
XX 10-JUN-1998; 98US-0088810.
XX 10-JUN-1998; 98US-0088811.
XX 10-JUN-1998; 98US-0088824.
XX 10-JUN-1998; 98US-0088825.
XX 10-JUN-1998; 98US-0088826.
XX 11-JUN-1998; 98US-0088858.
XX 11-JUN-1998; 98US-0088861.
XX 11-JUN-1998; 98US-0088863.
XX 12-JUN-1998; 98US-0088876.
XX 12-JUN-1998; 98US-0089090.
XX 16-JUN-1998; 98US-0089105.
XX 16-JUN-1998; 98US-0089440.
XX 16-JUN-1998; 98US-0089512.
XX 16-JUN-1998; 98US-0089514.
XX 17-JUN-1998; 98US-0089532.
XX 17-JUN-1998; 98US-0089538.
XX 17-JUN-1998; 98US-0089598.
XX 17-JUN-1998; 98US-0089599.
XX 17-JUN-1998; 98US-0089600.
XX 17-JUN-1998; 98US-0089653.
XX 18-JUN-1998; 98US-0089801.
XX 18-JUN-1998; 98US-0089907.
XX 18-JUN-1998; 98US-0089908.
XX 19-JUN-1998; 98US-0089947.
XX 19-JUN-1998; 98US-0089948.
XX 19-JUN-1998; 98US-0089952.
XX 22-JUN-1998; 98US-0090246.
XX 22-JUN-1998; 98US-0090252.
XX 22-JUN-1998; 98US-0090254.
XX 23-JUN-1998; 98US-0090349.
XX 23-JUN-1998; 98US-0090355.
XX 23-JUN-1998; 98US-0090357.
XX 24-JUN-1998; 98US-0090429.
XX 24-JUN-1998; 98US-0090431.
XX 24-JUN-1998; 98US-0090435.
XX 24-JUN-1998; 98US-0090444.
XX 24-JUN-1998; 98US-0090445.
XX 24-JUN-1998; 98US-0090461.
XX 24-JUN-1998; 98US-0090472.
XX 24-JUN-1998; 98US-0090535.
XX 24-JUN-1998; 98US-0090538.
XX 24-JUN-1998; 98US-0090540.
XX 24-JUN-1998; 98US-0090557.
XX 25-JUN-1998; 98US-0090676.
XX 25-JUN-1998; 98US-0090678.
XX 25-JUN-1998; 98US-0090688.
XX 25-JUN-1998; 98US-0090690.
XX 25-JUN-1998; 98US-0090691.

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PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096357.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
XX
PA (GENETECH ) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith Y, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI; 2000-072883/06.
DR

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DR N-PSDB; AA265059.
XX
XX Membrane-bound proteins and related nucleotide sequences -
PT
XX claim 12; Fig 208; 822pp; English.
PS
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes. In chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
XX Sequence 282 AA:
SQ

```

```

Query Match 90.9%; Score 1431; DB 21; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.6e-119;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 28 MASLGQILFWMSIISIIITAGATALTIGISGRHSITVTYVSAAGNIGDGLSCTFPP 87
DB 1 maslsgllfwstisllllagalaalllfglsgrhsiltvltvasagnigedgllsctfep 60
QY 88 DIKLSDIYQWLKEGYLGLVHEFEKDELSDEDEMERGRRTAVFAQOVIVGNASLRKLV 147
DB 61 dlklsdylvqlwkegyllglvhefkegkdelsegdenfgrtavrfaqvivgnaslrklnv 120
QY 148 QLTDAITYKCYITTSKGNANLEFYTGAFSPMEVVDVNASSETRCGAPRFPQPTVY 207
DB 121 qltadqlykcylltskqgnanleyktgafspmevvdvnaassetlrcgaprwpfpqpvv 180
QY 208 MASQVDOGANFSEVNTSFELNSENVTMKVSVLYVWTINNTYSCMIENDIKATGDIYV 267
DB 181 masqvdganfsevnstfelnsenvtmkvsvlyvwtlnntyscmiendikaagdlkv 240
QY 268 TESEIKRRSHLQILNSKASLCVSPFAISWALLPLSPYMLK 309
DB 241 teselkrshlqlnskaelcvssffaiswallplspylmk 282

```

```

RESULT 5
AAB99204
ID AAB99204 standard; Protein; 282 AA.
XX
XX AAB99204;
AC
XX 04-SEP-2001 (first entry)
DT
XX Human ovarian tumour-derived antigen OBE #1.
DE
XX
XX Cystostatic; human; breast tumour protein; breast cancer;
KM ovarian tumour; antigen; OBE.
XX
XX Homo sapiens.
OS
XX
XX WO200140269-A2.
PN
XX
XX 07-JUN-2001.
PD
XX
XX 29-NOV-2000; 2000WO-US32520.
PF
XX
XX 30-NOV-1999; 99US-0451651.
PR 22-FEB-2000; 2000US-0510662.
PR 10-MAR-2000; 2000US-0523586.

```


KW Human; secreted and transmembrane protein; PRO; cytosolic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US08439.
 XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04341.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrata N, Fong S, Gerber H, Gerlitsen ME, Goddard A, Godowski PJ,
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT,
 PI Zhang Z;
 XX
 DR WPI: 2001-032160/04.
 DR N-PSDB; AAF44205.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 208; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF444770 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 282 AA;

Best Local Similarity 100.0%; Pred. No. 9.6e-119;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 MASLGOILEWISIIIIIIIIAGAIALIIIGFCISGRHSITVTVTASAGNIGDGLSCFEP 87
 Db 1 maslqglllfwslslllllagaalallfgisgrhsitvtvtasagnigedgllscfep 60
 QY 88 DIKLSDIVIQWLKEGVGLVHEFEKGDSEODEMERGTAVFADQVYGNASLRLKNV 147
 Db 61 dlksdlvlgwlkegylgvlvhefkegkdelsedemfrgtavfadqvlgnaslrlknv 120
 QY 148 QLTDACTYKCYITTSKGNANLEKTAFAFMEVVDVNASSETLRCEAPRPFQPTVY 207
 Db 121 qltdaglykcyiltskqgnanlekytga fmpdevvdy nassetlrceaprfpqptvy 180
 QY 208 MASQVQGANFSEVNTSEFLNSENVTMKVSVLYVWTINNTSCMIENDIATGDIKY 267
 Db 181 masqvqganfsevsntseflnsenvtmkvsvlyvwtlnntyscmliendiakadiky 240
 QY 268 TSEIKRRSHLQILNSKASLCVSSFPFASWALPLSPYIMLK 309
 Db 241 teselkrrshlqlnksalcvssffalswalplspylimlk 282
 RESULT 8
 AAB60776
 ID AAB60776 standard; peptide: 195 AA.
 XX
 AC AAB60776;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Gene 47 related peptide #2.
 XX
 KW Secreted protein; gene therapy; vaccine; cancer; leukemia;
 KW autoimmune disease; allergy; inflammation; graft rejection;
 KW hyperproliferation; cardiovascular; infection.
 XX
 OS Homo sapiens.
 PN WO200076531-A1.
 XX
 PD 21-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-US15137.
 XX
 PR 11-JUN-1999; 99US-0138625.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM, Komatsoulis GA;
 PI WPI: 2001-071148/08.
 DR
 XX
 PT Nucleic acids encoding 47 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 PS Disclosure; Page 524-525; 525pp; English.
 XX
 CC The present invention relates to 26 secreted human proteins. The
 CC proteins may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate polypeptide expression.
 CC For example, they may be used in gene therapy or in vaccines.
 CC Typical of diseases which are potentially treatable are cancers
 CC (including leukemia), autoimmune diseases, allergies, inflammation,
 CC graft rejection, hyperproliferation, cardiovascular diseases
 CC (particularly critical limb ischemia and coronary disease) and any
 CC involving abnormal angiogenesis, neurodegeneration and/or
 CC infectious diseases.
 XX
 SQ Sequence 195 AA;

Query Match 90.9%; Score 1431; DB 22; Length 282;

CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angioedema disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein fragment referred to in the disclosure of the invention.
XX
XX Sequence 387 AA:
XQ

Query Match	15.68;	Score 246;	DB 22;	Length 387;
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Best Local Similarity 26.28; Pred. No. 1.2e-13;
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

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0Y 19 QJRMESPSPAMASLGOI-----LE--WSISIIIIILGAILITGECI---SCRHS 63
Db 28 eYfwdggdgvplIgtlvnttsgmanegglIdvshsIltvrvlgangtysclvrnplvqgdahs 87
0Y 64 IIVTVVAS-----AGNIGEDGILSCFE--EPDIRKSDIYIOMLRKGVLV 107
Db 88 vtlfpqpsltgavevqyrvpedvvalvaygdalchsfespepgfstqtnllhqltdetqvl 147
0Y 108 HEFKGKDELSDQDMFEGRTATVPADQVITVNASIRLKNQOLDNAGYKCYITTSKSGN 167
Db 148 hstfgird--qgsaayanrtalIpdllagqnaelrlqrvvadegsficf-vslrfdgs 202
0Y 168 ANLEKRTGA-FSMEPVANDVN-----ASSEFLREAPRMFPQPIVWASQDQANFSEV 222
Db 203 aavsvqvaapyskpmtlepkdrlrpdtdvtltcsyrygypbeaefw--qdgqgvplltgn 260
0Y 222 SNTSELSNSENVTMKRVSVLYNTV--INNTSQTMTENDIAK--ATGDIKVT 268
Db 261 vltv--qmanegglIdvshsIltvrvlgangtysclvrnplvqgdahqvstlc 309

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RESULT 11

ID	AAU00905	standard; Protein; 441 AA.
----	----------	----------------------------

AC AAU00905;

DT 23-MAY-2001 (first entry)

Human B lymphocyte activation antigen fragment, SEQ ID NO:4.

KW Human; B lymphocyte activation antigen; BLA4; B7 family;
KW immunoglobulin superfamily; T lymphocyte activation; immunogen;
KW antibody; immune response-associated disorder; cancer; HIV;
KW autoimmune disorder; organ transplantation; bacterial infection;
KW viral infection; fungal infection; mycobacterial infection;
KW human immunodeficiency virus; hepatitis virus; herpes virus;
KW mycobacterial infection; autoimmune disorder; malaria; candidiasis;
KW connective tissue disease; multiple sclerosis; rheumatoid arthritis;
KW systemic lupus erythematosus; autoimmune pulmonary inflammation;
KW autoimmune thyroiditis; diabetes mellitus; myasthenia gravis;
KW autoimmune inflammatory eye disease; psoriasis; fertility; metabolism;
KW analgesic; hyperproliferative disorder.

05 Homo sapiens.

PN WO200118204-A1.

PD 15-MAR-2001.

XX

PF 31-AUG-2000; 2000WO-US24220.

PR 03-SEP-1999; 99US-0152383.

PR 18-FEB-2000; 2000US-0183578.

XX	500000	100000	00
XX	500000	100000	00

PA (BIOJ) BIOGEN INC.

PI Green C, Kotelanski V, De

DR WPT; 2001-226745/23.

[illegible]

polynucleotide for diagnosis

PT autoimmune disorders -

PS Claim 10; Fig '2; 102pp; Eng1

The sequence is a fragment of a human B lymphocyte activation antigen, BLAA, which is a member of the B7 family of B lymphocyte antigens. Like other members of the B7 family, BLAA is a member of the immunoglobulin (Ig) superfamily. The present sequence is a fragment of a BLAA protein which has three Ig-like domains followed by a transmembrane domain and a 44 amino acid cytoplasmic domain. BLAA functions by binding to activated T lymphocytes and providing signals for T lymphocyte cell growth and activation. BLAA proteins, polynucleotides encoding them and antibodies raised against them are useful for treating or preventing an immune response-associated disorder and in the manufacture of a medicament for treating a syndrome associated with a human disease. BLAA proteins and polynucleotides are useful for determining the presence or predisposition to a disease associated with altered levels of a BLAA polypeptide or polynucleotide. BLAA proteins and polynucleotides are useful for modulating immune responses and in the treatment of cancers, infectious diseases, autoimmune disorders and complications associated with graft vs. host disease in organ transplantation. Immune deficiencies may be genetic or viral, resulting from bacterial or fungal infections including infections by Human Immunodeficiency virus (HIV), hepatitis viruses, herpes viruses, mycobacteria, malaria and candidiasis. Autoimmune disorders include connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis and autoimmune inflammatory eye disease. BLAA nucleic acid molecules, proteins and antibodies are useful in screening assays, detection assays including chromosomal mapping, tissue typing, forensic biology and in diagnostic and prognostic assays. In addition, BLAA polypeptides also inhibit microbial growth, affect bodily characteristics (e.g hair colour, height and weight), fertility, metabolism (e.g of fat, lipid or protein) provide analgesic or pain relieving effects and treat deficiency related diseases and hyperproliferative disorders, such as psoriasis.

Sequence 441 AA;

Query Match	15.68;	Score 246;	DB 22;	Length 441;
-------------	--------	------------	--------	-------------

Matches	76;	Conservative	55;	Mismatches	111;	Indels	48;	Gaps	13;
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0Y 19 QIRREPSPMASLIGQI-----LF--WSIIIIIIILAGALIIIGGT---SGRHS 63
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 82 evfmgdgqgvplctgnvtscsmanegqifdvhsllrvlrgangfysclrnprvlqdahs 141
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
0Y 64 ITVTVAS-----AGNIGEDSILSCTF--EEDIKLSDIVIOMLKEGVGLV 107
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 142 vtlpqrsptgavevqvpdpvvalvytdctllhcsfpepgfsaltqinllwqltdckqlv 201
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
0Y 108 HEFEKGEDELSEQDEMRGRTAFVADQIVYINMSLRKNQLNDACTGYKCIITTSKGN 167
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 202 hstfegcd-----qgsaantaltlfpdlagnasnlrlqrvadesgfctf-vslrdfs 256
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OY 168 ANLEYKTGA-FSMPEVNDVN-----ASSETLRCEAPRMPPTVYVWASQVDOGANFSEV 221
 DB 257 aavslqvaapyskpsmlepnkdlrpgdvtlccssyrygpeeevfw--qdgsgvplgtm 314
 OY 222 SNTSFEIENSENVTKKVSVLVYNTV-INNTYSCHIENDIAK--ATGDIKVT 268
 DB 315 vltss-qmanegqlfdvhsylrvvlgangtysclvrnpvlgdghsvtl 363

RESULT 12
 AAU00906
 ID AAU00906 standard; Protein; 534 AA.

AC AAU00906;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE Human B lymphocyte activation antigen A7, BLAA#3.
 XX
 KW Human; B lymphocyte activation antigen; BLAA; B7 family;
 KW Immunoglobulin superfamily; T lymphocyte activation; immunogen;
 KW antibody; immune response-associated disorder; cancer; HIV;
 KW autoimmune disorder; organ transplantation; bacterial infection;
 KW viral infection; fungal infection; mycobacterial infection;
 KW human immunodeficiency virus; hepatitis virus; herpes virus;
 KW mycobacterial infection; autoimmune disorder; malaria; candidiasis;
 KW connective tissue disease; multiple sclerosis; rheumatoid arthritis;
 KW systemic lupus erythematosus; autoimmune pulmonary inflammation;
 KW autoimmune thyroiditis; diabetes mellitus; myasthenia gravis;
 KW autoimmune inflammatory eye disease; psoriasis; fertility; metabolism;
 KW analgesic; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200118204-A1.
 XX
 PD 15-MAR-2001.
 XX
 PE 31-AUG-2000; 2000WO-US24220.
 XX
 PR 03-SEP-1999; 99US-0152383.
 PR 21-DEC-1999; 99US-0172909.
 PR 18-FEB-2000; 2000US-0183578.
 PR 30-AUG-2000; 2000US-0651200.
 XX
 PA (CURA-) CURAGEN CORP.
 PA (BIOJ) BIOGEN INC.
 XX
 PI Green C, Kotelanski V, De Fougerolles A, Carulli J, Hession C;
 XX
 DR WPI: 2001-226745/23.
 DR N-PSDB: AAS00875.
 XX
 PT Novel human B lymphocyte activation antigen B7 family polypeptide,
 PT polynucleotide for diagnosis, prevention, treatment of immune
 PT response-associated disorders such as cancer, infectious diseases,
 PT autoimmune disorders
 XX
 PS Claim 10; Fig 3; 102pp; English.
 XX
 CC The sequence is a human B lymphocyte activation antigen, BLAA,
 CC which is a member of the B7 family of B lymphocyte antigens. Like
 CC other members of the B7 family, BLAA is a member of the Immunoglobulin
 CC (Ig) superfamily. The present sequence is a BLAA protein which
 CC has four Ig-like domains, followed by a transmembrane domain and a 44
 CC amino acid cytoplasmic domain. BLAA functions by binding to activated
 CC T lymphocytes and providing signals for T lymphocyte cell growth and
 CC activation. BLAA proteins, polynucleotides encoding them and
 CC antibodies raised against them are useful for treating or preventing an
 CC immune response-associated disorder and in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. BLAA
 CC proteins and polynucleotides are useful for determining the presence or

CC predisposition to a disease associated with altered levels of a BLAA
 CC polypeptide or polynucleotide. BLAA proteins and polynucleotides and are
 CC useful for modulating immune responses and in the treatment of cancers,
 CC infectious diseases, autoimmune disorders and complications associated
 CC with graft vs. host disease in organ transplantation. Immune deficiencies
 CC may be genetic or viral, resulting from bacterial or fungal infections
 CC including infections by Human immunodeficiency virus (HIV), hepatitis
 CC viruses, herpes viruses, mycobacteria, malaria and candidiasis.
 CC Autoimmune disorders include connective tissue disease, multiple
 CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
 CC pulmonary inflammation, autoimmune thyroiditis, insulin dependent
 CC diabetes mellitus, myasthenia gravis and autoimmune inflammatory eye
 CC disease. BLAA nucleic acid molecules, proteins and antibodies are useful
 CC in screening assays, detection assays including chromosomal mapping,
 CC tissue typing, forensic biology and in diagnostic and prognostic assays.
 CC In addition, BLAA polypeptides also inhibit microbial growth, affect
 CC bodily characteristics (e.g. hair colour, height and weight), fertility,
 CC metabolism (e.g. of fat, lipid or protein) provide analgesic or pain
 CC releasing effects and treat deficiency related diseases and
 CC hyperproliferative disorders, such as psoriasis.

XX
 S0 Sequence 534 AA;

Query Match 15.6%; Score 246; DB 22; Length 534;
 Best Local Similarity 26.2%; Pred. No. 1.9e-13;
 Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

OY 19 QIRMEPSPMASIGOI-----LF--WSIIISIIILAGAILIGGI--SGRHS 63
 DB 175 evltwqdgqgypilgnvtlsgtmanegqlfdvhsllrvvlgangtysclvrnpvlgdghs 234
 OY 64 ITVTYVAS-----AGNIGEDGILSCTF--EPDILSDIVIOMKEGVGLV 107
 DB 235 vltlprspfgavevqpedgvvalvgtldatlccsfspgfslaqlnllwqltdckqly 294
 OY 108 HEFKEGDELSEODEMRGRTAVFAPOVITGNASLRLKNVQLDAGYKCYITTSKSGKN 167
 DB 295 hsftegrd-----qgsayantalfpdliaqnasllrqrvaegsfctf-vsltdfsg 349
 OY 168 ANLEYKTGA-FSMPEVNDVN-----ASSETLRCEAPRMPPTVYVWASQVDOGANFSEV 221
 DB 350 aavslqvaapyskpsmlepnkdlrpgdvtlccssyrygpeeevfw--qdgsgvplgtm 407
 OY 222 SNTSFEIENSENVTKKVSVLVYNTV-INNTYSCHIENDIAK--ATGDIKVT 268
 DB 408 vltss-qmanegqlfdvhsylrvvlgangtysclvrnpvlgdghsvtl 456

RESULT 13
 AAB88459
 ID AAB88459 standard; Protein; 534 AA.
 XX
 AC AAB88459;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE Human membrane or secretory protein clone PSEC0249.
 XX
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;
 KW rheumatoid arthritis; diabetes.
 XX
 OS Homo sapiens.
 XX
 PN EP1067182-A2.
 XX
 PD 10-JAN-2001.
 XX
 PE 07-JUL-2000; 2000EP-0114090.
 XX
 PR 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-0118775.
 PR 02-MAY-2000; 2000JP-0183766.

22-OCT-2001 (first entry)

DE XX Human polypeptide SEQ ID NO 2941.

XX XX Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokine; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX XX Homo sapiens.

OS OS WO200153312-A1.

XX XX 26-JUL-2001.

XX XX 26-DEC-2000; 2000WO-US34263.

XX XX 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX XX (HYSE-) HYSEQ INC.

XX XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX XX WPI: 2001-442253/47.

DR N-PSDB: AAI58952.

XX XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

XX XX Example 4; SEQ ID NO 2941; 10078bp; English.

XX XX The invention relates to human nucleic acids (AAI5798-AAI61369) and

CC the encoded polypeptides (AAM386A2-AAM4213) with nootropic,

CC immunosuppressant and cyostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

CC XX

XX XX Sequence 1020 AA;

SQ

Query Match 15.6%, Score 246; DB 22; Length 1020;

Best Local Similarity 26.2%, Pred. No. 4.8e-13;

Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

OY 19 QIRWEPSPAMASLGOI-----LF--WSIIIIIIAGALALIGFGI---SGRHS 63

DB 567 efwgdgggvpplgnvtsgmanegllfdvhsilrvlgangtyclvrnpvlgqdaahs 626

OY 64 ITVTIVAS-----AGNIGEDGILSCF--EPDIKLSDIYIOWLKEGVLGV 107

DB 627 vtltpgrptgavveqvpedpvvalvgtdatlrscfspepfsagqlnliqldtkqlv 686

OY 108 HEFRKGDLSRODEMFRGRTAVFADQYIVGNASRLKNVOLTDACTYKCYIIITSKGN 167

DB 687 hstlegtd---qgsayanrtallfpdliaqnaslrlqrvvadegstfct-vslrddfgs 741

OY 168 ANLEKRTGA-FSPPEVNVQYN-----ASSETLRCEAPWFPQPTVWMAQVDGAFSEV 221

DB 742 aavslqvaapykspsmtlepknklrpgdtvtltcssyrgypeaevf--qdgqgvpplgn 799

OY 222 SNTSPELSENVTMKRVSVLYNVT-INNTYSCEIENDIAK--ATGDIAVT 268

DB 800 vltsgmanegllfdvhsilrvlgangtyclvrnpvlgqdaahs vlt 848

Search completed: February 15, 2002, 14:20:18

Job time: 83 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 15, 2002, 14:19:00 ; Search time 96.49 Seconds
(Without alignments)
889.170 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574

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BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/paa/US082.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1574	100.0	309	US-09-404-879A-392
2	1574	100.0	309	US-09-617-747-392
3	1574	100.0	309	US-09-636-801-392
4	1574	100.0	309	US-09-667-857-392
5	1574	100.0	309	US-09-778-320-209
6	1574	100.0	309	US-09-827-271-392
7	1574	100.0	309	US-09-884-441-392
8	1574	100.0	309	US-09-907-969-392
9	1574	100.0	309	US-09-910-689-209

10	1431	90.9	282	1	PCT-US01-20917-14	Sequence 14, Appl
11	1431	90.9	282	1	PCT-US01-41430-5	Sequence 5, Appl
12	1431	90.9	282	18	US-09-404-879A-393	Sequence 393, App
13	1431	90.9	282	20	US-09-617-747-393	Sequence 393, App
14	1431	90.9	282	20	US-09-636-801-393	Sequence 393, App
15	1431	90.9	282	20	US-09-667-857-393	Sequence 393, App
16	1431	90.9	282	21	US-09-709-238-291	Sequence 291, App
17	1431	90.9	282	21	US-09-778-320-208	Sequence 208, App
18	1431	90.9	282	22	US-09-827-271-393	Sequence 393, App
19	1431	90.9	282	22	US-09-850-178-33	Sequence 33, Appl
20	1431	90.9	282	22	US-09-884-441-393	Sequence 393, Appl
21	1431	90.9	282	22	US-09-896-738-2	Sequence 2, Appl
22	1431	90.9	282	23	US-09-907-969-393	Sequence 393, App
23	1431	90.9	282	23	US-09-910-689-208	Sequence 208, App
24	1431	90.9	282	23	US-09-929-769-8	Sequence 8, Appl
25	1431	90.9	282	23	US-09-941-992-291	Sequence 291, App
26	1431	90.9	282	23	US-09-950-083-5199	Sequence 5199, Ap
27	1320	83.9	255	22	US-09-896-738-3	Sequence 27, Appl
28	1295	82.3	255	1	PCT-US01-20917-28	Sequence 28, Appl
29	1184	75.2	231	1	PCT-US01-20917-28	Sequence 19, Appl
30	1163	73.9	227	1	PCT-US01-41430-19	Sequence 519, App
31	857.5	54.5	204	24	US-60-207-216-519	Sequence 132, App
32	842.5	53.5	195	1	PCT-US00-15137-132	Sequence 2748, Ap
33	665	42.2	152	24	US-60-195-053-2748	Sequence 7, Appl
34	593	37.7	116	22	US-09-896-738-7	Sequence 8, Appl
35	484	30.7	93	22	US-09-896-738-8	Sequence 5128, Ap
36	480	30.5	94	24	US-60-169-840-5128	Sequence 3684, Ap
37	480	30.5	94	24	US-60-169-868-3684	Sequence 3493, Ap
38	434	27.6	84	24	US-60-160-209-2463	Sequence 2463, Ap
39	434	27.6	84	24	US-60-160-209-2463	Sequence 415, App
40	348	22.1	65	20	US-09-617-747-415	Sequence 415, App
41	348	22.1	65	20	US-09-636-801-415	Sequence 415, App
42	348	22.1	65	20	US-09-667-857-415	Sequence 415, App
43	348	22.1	65	22	US-09-827-271-415	Sequence 415, App
44	348	22.1	65	22	US-09-884-441-415	Sequence 415, App
45	348	22.1	65	23	US-09-907-969-415	Sequence 415, App

ALIGNMENTS

RESULT 1
US-09-404-879A-392
: Sequence 392, Application US/09404879A
: GENERAL INFORMATION:
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: King, Gordon E.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.462C2
: CURRENT APPLICATION NUMBER: US/09/404,879A
: CURRENT FILING DATE: 1999-09-24
: NUMBER OF SEQ ID NOS: 393
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 392
: LENGTH: 309
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-404-879A-392

Query Match	100.0%	Score 1574:	DB 18:	Length 309:
Best Local Similarity	100.0%	Pred. No. 5.3e-152:		
Matches 309:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
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Db	1	HASAHASGRQLHSASTQIRMPSPAMASGQILFNSIIIIIIAGAILIIGFISG	60	
QY	61	RHSITVTTVASAGNIGEDGILSCFEPDIKLSDIVIOMLKGVGLVHEFRGDELSQ	120	
Db	61	RHSITVTTVASAGNIGEDGILSCFEPDIKLSDIVIOMLKGVGLVHEFRGDELSQ	120	

NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 392
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-667-857-392

Query Match 100.0%; Score 1574; DB 20; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 HASAHASGRORQLHSASQIRWEPSPAMASLGQILFWSITITITLGAIALIIGFGISG 60
QY 61 RHSITVTTVASAGNIGEDGILSCFTEPDIKLSIDIVIQWLKRGVGLVHEFEKGDSEQ 120
DB 61 RHSITVTTVASAGNIGEDGILSCFTEPDIKLSIDIVIQWLKRGVGLVHEFEKGDSEQ 120
QY 121 DEMFRGRTAVPADQYIVGNASLRKKNVQLTAGTYKCYIITSKGNANLEKTKGAFSMP 180
DB 121 DEMFRGRTAVPADQYIVGNASLRKKNVQLTAGTYKCYIITSKGNANLEKTKGAFSMP 180
QY 181 EVNVDYNASSSETLRCEARWFPQPTVWASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
DB 181 EVNVDYNASSSETLRCEARWFPQPTVWASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
QY 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHQLNSKASLCVSSFFAISMAL 300
DB 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHQLNSKASLCVSSFFAISMAL 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

RESULT 5

US-09-778-320-209
Sequence 209, Application US/09778320
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yuguo
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C5
CURRENT APPLICATION NUMBER: US/09/778.320
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 209
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-778-320-209

Query Match 100.0%; Score 1574; DB 21; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 RHSITVTTVASAGNIGEDGILSCFTEPDIKLSIDIVIQWLKRGVGLVHEFEKGDSEQ 120

DB 61 RHSITVTTVASAGNIGEDGILSCFTEPDIKLSIDIVIQWLKRGVGLVHEFEKGDSEQ 120
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DB 121 DEMFRGRTAVPADQYIVGNASLRKKNVQLTAGTYKCYIITSKGNANLEKTKGAFSMP 180
QY 181 EVNVDYNASSSETLRCEARWFPQPTVWASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
DB 181 EVNVDYNASSSETLRCEARWFPQPTVWASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
QY 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHQLNSKASLCVSSFFAISMAL 300
DB 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHQLNSKASLCVSSFFAISMAL 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

RESULT 6

US-09-827-271-392
Sequence 392, Application US/09827271
GENERAL INFORMATION:
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C6
CURRENT APPLICATION NUMBER: US/09/827.271
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 392
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-827-271-392

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Best Local Similarity 100.0%; Pred. No. 5.3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 HASAHASGRORQLHSASQIRWEPSPAMASLGQILFWSITITITLGAIALIIGFGISG 60
QY 61 RHSITVTTVASAGNIGEDGILSCFTEPDIKLSIDIVIQWLKRGVGLVHEFEKGDSEQ 120
DB 61 RHSITVTTVASAGNIGEDGILSCFTEPDIKLSIDIVIQWLKRGVGLVHEFEKGDSEQ 120
QY 121 DEMFRGRTAVPADQYIVGNASLRKKNVQLTAGTYKCYIITSKGNANLEKTKGAFSMP 180
DB 121 DEMFRGRTAVPADQYIVGNASLRKKNVQLTAGTYKCYIITSKGNANLEKTKGAFSMP 180
QY 181 EVNVDYNASSSETLRCEARWFPQPTVWASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
DB 181 EVNVDYNASSSETLRCEARWFPQPTVWASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
QY 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHQLNSKASLCVSSFFAISMAL 300
DB 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHQLNSKASLCVSSFFAISMAL 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

RESULT 7

US-09-884-441-392
Sequence 392, Application US/09884441
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.

```

; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 392
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-392

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Query Match          100.0%; Score 1574; DB 22; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HASAHASGRQRLHSASTQIRMEPPSPAMASLGQILFWSIISIIIIILAGATALLIGFGISG 60
   1 HASAHASGRQRLHSASTQIRMEPPSPAMASLGQILFWSIISIIIIILAGATALLIGFGISG 60
DB 1 HASAHASGRQRLHSASTQIRMEPPSPAMASLGQILFWSIISIIIIILAGATALLIGFGISG 60
QY 61 RHSITVTYVASAGNIGEDGILSCTFEPPDIKLSDIVIOWLKEGVGLVHEFEKGDLSQ 120
   61 RHSITVTYVASAGNIGEDGILSCTFEPPDIKLSDIVIOWLKEGVGLVHEFEKGDLSQ 120
DB 61 RHSITVTYVASAGNIGEDGILSCTFEPPDIKLSDIVIOWLKEGVGLVHEFEKGDLSQ 120
QY 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
   121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
DB 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
QY 181 EVVNDYNASSETLRCEAPRFPOPTYVMAASQVQGANFSEVNTSEFNSENVTMAYVSV 240
   181 EVVNDYNASSETLRCEAPRFPOPTYVMAASQVQGANFSEVNTSEFNSENVTMAYVSV 240
DB 181 EVVNDYNASSETLRCEAPRFPOPTYVMAASQVQGANFSEVNTSEFNSENVTMAYVSV 240
QY 241 LYVNTINNTYSCMIENDIAKATGDIKYTESEIKRSHLQLLNSKASLCVSSFFAISMALL 300
   241 LYVNTINNTYSCMIENDIAKATGDIKYTESEIKRSHLQLLNSKASLCVSSFFAISMALL 300
DB 241 LYVNTINNTYSCMIENDIAKATGDIKYTESEIKRSHLQLLNSKASLCVSSFFAISMALL 300
QY 301 PLSPLYMLK 309
   301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

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RESULT 8

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US-09-907-969-392
; Sequence 392, Application US/09907969
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Hill, Paul
; APPLICANT: Albone, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 392
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-969-392

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Query Match          100.0%; Score 1574; DB 23; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HASAHASGRQRLHSASTQIRMEPPSPAMASLGQILFWSIISIIIIILAGATALLIGFGISG 60
   1 HASAHASGRQRLHSASTQIRMEPPSPAMASLGQILFWSIISIIIIILAGATALLIGFGISG 60
DB 1 HASAHASGRQRLHSASTQIRMEPPSPAMASLGQILFWSIISIIIIILAGATALLIGFGISG 60
QY 61 RHSITVTYVASAGNIGEDGILSCTFEPPDIKLSDIVIOWLKEGVGLVHEFEKGDLSQ 120
   61 RHSITVTYVASAGNIGEDGILSCTFEPPDIKLSDIVIOWLKEGVGLVHEFEKGDLSQ 120
DB 61 RHSITVTYVASAGNIGEDGILSCTFEPPDIKLSDIVIOWLKEGVGLVHEFEKGDLSQ 120
QY 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
   121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
DB 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
QY 181 EVVNDYNASSETLRCEAPRFPOPTYVMAASQVQGANFSEVNTSEFNSENVTMAYVSV 240
   181 EVVNDYNASSETLRCEAPRFPOPTYVMAASQVQGANFSEVNTSEFNSENVTMAYVSV 240
DB 181 EVVNDYNASSETLRCEAPRFPOPTYVMAASQVQGANFSEVNTSEFNSENVTMAYVSV 240
QY 241 LYVNTINNTYSCMIENDIAKATGDIKYTESEIKRSHLQLLNSKASLCVSSFFAISMALL 300
   241 LYVNTINNTYSCMIENDIAKATGDIKYTESEIKRSHLQLLNSKASLCVSSFFAISMALL 300
DB 241 LYVNTINNTYSCMIENDIAKATGDIKYTESEIKRSHLQLLNSKASLCVSSFFAISMALL 300
QY 301 PLSPLYMLK 309
   301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

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RESULT 9

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US-09-910-689-209
; Sequence 209, Application US/09910689
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-689-209

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Query Match          100.0%; Score 1574; DB 23; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HASAHASGRQRLHSASTQIRMEPPSPAMASLGQILFWSIISIIIIILAGATALLIGFGISG 60
   1 HASAHASGRQRLHSASTQIRMEPPSPAMASLGQILFWSIISIIIIILAGATALLIGFGISG 60
DB 1 HASAHASGRQRLHSASTQIRMEPPSPAMASLGQILFWSIISIIIIILAGATALLIGFGISG 60
QY 61 RHSITVTYVASAGNIGEDGILSCTFEPPDIKLSDIVIOWLKEGVGLVHEFEKGDLSQ 120
   61 RHSITVTYVASAGNIGEDGILSCTFEPPDIKLSDIVIOWLKEGVGLVHEFEKGDLSQ 120
DB 61 RHSITVTYVASAGNIGEDGILSCTFEPPDIKLSDIVIOWLKEGVGLVHEFEKGDLSQ 120
QY 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
   121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
DB 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
QY 181 EVVNDYNASSETLRCEAPRFPOPTYVMAASQVQGANFSEVNTSEFNSENVTMAYVSV 240
   181 EVVNDYNASSETLRCEAPRFPOPTYVMAASQVQGANFSEVNTSEFNSENVTMAYVSV 240

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; Db 181 EVAVDYNASSETLRCEAPRMPQPTVYVWASQVDOGANFSEVNTSEFELNSENVTMKVSV 240
;
; QY 241 LVAVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLLNSKASLCVSSFFAISMALL 300
;
; Db 241 LVAVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLLNSKASLCVSSFFAISMALL 300
;
; QY 301 PLSPLYMLK 309
;
; Db 301 PLSPLYMLK 309
;
; RESULT 10
; PCT-US01-20917-14
; Sequence 14, Application PC/TUS0120917
;
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: B7-Like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT124PCT
; CURRENT APPLICATION NUMBER: PCT/US01/20917
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US01-20917-14

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Query Match 90.9%; Score 1431; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.1e-137;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 28 MASLQGLFWSIIIIIIIIAGATALLIGFISGRHSITVTYVWASAGNIGEDGILSCFEP 87
;
; Db 1 MASLQGLFWSIIIIIIIIAGATALLIGFISGRHSITVTYVWASAGNIGEDGILSCFEP 60
;
; QY 88 DIKLSDIVIOMLKEGVGLVHEFEKDESEODEMRGRTAFADQVIYGNASLRKLV 147
;
; Db 61 DIKLSDIVIOMLKEGVGLVHEFEKDESEODEMRGRTAFADQVIYGNASLRKLV 120
;
; QY 148 QLTDACTYKCYIITSKGGANLEKYGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 207
;
; Db 121 QLTDACTYKCYIITSKGGANLEKYGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 180
;
; QY 208 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 267
;
; Db 181 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 240
;
; QY 268 TESEIKRRSHLQLLNSKASLCVSSFFAISMALLPLSPYMLK 309
;
; Db 241 TESEIKRRSHLQLLNSKASLCVSSFFAISMALLPLSPYMLK 282
;
; RESULT 11
; PCT-US01-41430-5
; Sequence 5, Application PC/TUS0141430
;
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE REFERENCE: 07039-219M01
; CURRENT APPLICATION NUMBER: PCT/US01/41430
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5

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; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US01-41430-5

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Query Match 90.9%; Score 1431; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.1e-137;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; QY 28 MASLQGLFWSIIIIIIIIAGATALLIGFISGRHSITVTYVWASAGNIGEDGILSCFEP 87
;
; Db 1 MASLQGLFWSIIIIIIIIAGATALLIGFISGRHSITVTYVWASAGNIGEDGILSCFEP 60
;
; QY 88 DIKLSDIVIOMLKEGVGLVHEFEKDESEODEMRGRTAFADQVIYGNASLRKLV 147
;
; Db 61 DIKLSDIVIOMLKEGVGLVHEFEKDESEODEMRGRTAFADQVIYGNASLRKLV 120
;
; QY 148 QLTDACTYKCYIITSKGGANLEKYGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 207
;
; Db 121 QLTDACTYKCYIITSKGGANLEKYGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 180
;
; QY 208 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 267
;
; Db 181 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 240
;
; QY 268 TESEIKRRSHLQLLNSKASLCVSSFFAISMALLPLSPYMLK 309
;
; Db 241 TESEIKRRSHLQLLNSKASLCVSSFFAISMALLPLSPYMLK 282
;
; RESULT 12
; US-09-404-879A-393
; Sequence 393, Application US/09404879A
;
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-404-879A-393

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Query Match 90.9%; Score 1431; DB 18; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.1e-137;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; QY 28 MASLQGLFWSIIIIIIIIAGATALLIGFISGRHSITVTYVWASAGNIGEDGILSCFEP 87
;
; Db 1 MASLQGLFWSIIIIIIIIAGATALLIGFISGRHSITVTYVWASAGNIGEDGILSCFEP 60
;
; QY 88 DIKLSDIVIOMLKEGVGLVHEFEKDESEODEMRGRTAFADQVIYGNASLRKLV 147
;
; Db 61 DIKLSDIVIOMLKEGVGLVHEFEKDESEODEMRGRTAFADQVIYGNASLRKLV 120
;
; QY 148 QLTDACTYKCYIITSKGGANLEKYGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 207
;
; Db 121 QLTDACTYKCYIITSKGGANLEKYGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 180
;
; QY 208 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 267
;
; Db 181 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 240
;
; QY 268 TESEIKRRSHLQLLNSKASLCVSSFFAISMALLPLSPYMLK 309

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Db 241 TSEIKRSHLOLNKSKASLCVSSFFAISWALLPLSPYLMK 282

RESULT 13

US-09-617-747-393

Sequence 393, Application US/09617747
 GENERAL INFORMATION:
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: King, Gordon E.
 APPLICANT: Algate, Paul A.
 APPLICANT: Fling, Steven P.
 APPLICANT: Retter, Marc W.
 APPLICANT: Fanger, Gary Richard
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.462C3
 CURRENT APPLICATION NUMBER: US/09/617,747
 CURRENT FILING DATE: 2000-07-17
 NUMBER OF SEQ ID NOS: 455
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 393
 LENGTH: 282
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-617-747-393

Query Match 90.9%; Score 1431; DB 20; Length 282;
 Best Local Similarity 100.0%; Pred. No. 2.1e-137;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWSIIITIIAGALALIIIGFISGRHSITVTYVVASAGNIGEDGILSTCEP 87
 Db 1 MASLGQILFWSIIITIIAGALALIIIGFISGRHSITVTYVVASAGNIGEDGILSTCEP 60
 -QY 88 DIKLSDIYQWLKEGVLGVHEFEKDELSEODEMFRGRTAVFADQYIVGNASLRKNV 147
 Db 61 DIKLSDIYQWLKEGVLGVHEFEKDELSEODEMFRGRTAVFADQYIVGNASLRKNV 120
 QY 148 QLTDACTYKCYITTSKGNANLEKYGAFSMPEVNDYNASSETLRCEAPRMFPQPTV 207
 Db 121 QLTDACTYKCYITTSKGNANLEKYGAFSMPEVNDYNASSETLRCEAPRMFPQPTV 180
 QY 208 WASQVDQANFSEVNTSEFELSENVTMKVSVLYVNTINNTYSCHIENDIAKATGDIK 267
 Db 181 WASQVDQANFSEVNTSEFELSENVTMKVSVLYVNTINNTYSCHIENDIAKATGDIK 240
 QY 268 TSEIKRSHLOLNKSKASLCVSSFFAISWALLPLSPYLMK 309
 Db 241 TSEIKRSHLOLNKSKASLCVSSFFAISWALLPLSPYLMK 282

RESULT 14

US-09-636-801-393

Sequence 393, Application US/09636801
 GENERAL INFORMATION:
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: King, Gordon E.
 APPLICANT: Algate, Paul A.
 APPLICANT: Fling, Steven P.
 APPLICANT: Retter, Marc W.
 APPLICANT: Fanger, Gary Richard
 APPLICANT: Reed, Steven G.
 APPLICANT: Vedyick, Thomas S.
 APPLICANT: Carter, Darick
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.462C4
 CURRENT APPLICATION NUMBER: US/09/636,801
 CURRENT FILING DATE: 2000-08-10
 NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 393
 LENGTH: 282
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-636-801-393

Query Match 90.9%; Score 1431; DB 20; Length 282;
 Best Local Similarity 100.0%; Pred. No. 2.1e-137;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWSIIITIIAGALALIIIGFISGRHSITVTYVVASAGNIGEDGILSTCEP 87
 Db 1 MASLGQILFWSIIITIIAGALALIIIGFISGRHSITVTYVVASAGNIGEDGILSTCEP 60
 QY 88 DIKLSDIYQWLKEGVLGVHEFEKDELSEODEMFRGRTAVFADQYIVGNASLRKNV 147
 Db 61 DIKLSDIYQWLKEGVLGVHEFEKDELSEODEMFRGRTAVFADQYIVGNASLRKNV 120
 QY 148 QLTDACTYKCYITTSKGNANLEKYGAFSMPEVNDYNASSETLRCEAPRMFPQPTV 207
 Db 121 QLTDACTYKCYITTSKGNANLEKYGAFSMPEVNDYNASSETLRCEAPRMFPQPTV 180
 QY 208 WASQVDQANFSEVNTSEFELSENVTMKVSVLYVNTINNTYSCHIENDIAKATGDIK 267
 Db 181 WASQVDQANFSEVNTSEFELSENVTMKVSVLYVNTINNTYSCHIENDIAKATGDIK 240
 QY 268 TSEIKRSHLOLNKSKASLCVSSFFAISWALLPLSPYLMK 309
 Db 241 TSEIKRSHLOLNKSKASLCVSSFFAISWALLPLSPYLMK 282

RESULT 15

US-09-667-857-393

Sequence 393, Application US/09667857
 GENERAL INFORMATION:
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: King, Gordon E.
 APPLICANT: Algate, Paul A.
 APPLICANT: Fling, Steven P.
 APPLICANT: Retter, Marc W.
 APPLICANT: Fanger, Gary Richard
 APPLICANT: Reed, Steven G.
 APPLICANT: Vedyick, Thomas S.
 APPLICANT: Carter, Darick
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.462C5
 CURRENT APPLICATION NUMBER: US/09/667,857
 CURRENT FILING DATE: 2000-09-20
 NUMBER OF SEQ ID NOS: 455
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 393
 LENGTH: 282
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-667-857-393

Query Match 90.9%; Score 1431; DB 20; Length 282;
 Best Local Similarity 100.0%; Pred. No. 2.1e-137;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWSIIITIIAGALALIIIGFISGRHSITVTYVVASAGNIGEDGILSTCEP 87
 Db 1 MASLGQILFWSIIITIIAGALALIIIGFISGRHSITVTYVVASAGNIGEDGILSTCEP 60
 QY 88 DIKLSDIYQWLKEGVLGVHEFEKDELSEODEMFRGRTAVFADQYIVGNASLRKNV 147
 Db 61 DIKLSDIYQWLKEGVLGVHEFEKDELSEODEMFRGRTAVFADQYIVGNASLRKNV 120
 QY 148 QLTDACTYKCYITTSKGNANLEKYGAFSMPEVNDYNASSETLRCEAPRMFPQPTV 207

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Db      121  QLTDACTYKCYIITSKSGNANLEKGTGAFSMPENVNDYNASSETLRCEAPRWFQPTVY 180
QY      208  WASOVDOGANFSEVSNTSFEINSENVMTMKVSVLYNVTINNYSCTIENDIAKATGDIKY 267
Db      181  WASOVDOGANFSEVSNTSFEINSENVMTMKVSVLYNVTINNYSCTIENDIAKATGDIKY 240
QY      268  TSEIIRRRSHQLLNSKASLCVSSFFAISWALLPLSPYMLK 309
Db      241  TSEIIRRRSHQLLNSKASLCVSSFFAISWALLPLSPYMLK 282

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Search completed: February 15, 2002, 14:22:24
 Job time: 204 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2002, 14:19:50 ; Search time 24.44 Seconds
(without alignments)
1849.351 Million cell updates/sec

Title: US-09-636-801-392
Perfect score: 1574
Sequence: 1 HASAHASGRQLRHASSTQI.....SSFAISNALLPLSPYLMK 309

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_oranelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rudent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1425	90.5	282	4	09H6B2 homo sapien
2	247	15.7	316	4	09BXR1 homo sapien
3	225	14.3	220	4	09NM06
4	225	14.3	414	4	09UM44
5	223	14.2	513	4	000481
6	223	14.2	513	4	09HCY1
7	222.5	14.1	347	4	09H730
8	220	14.0	280	13	073716
9	219.5	13.9	286	6	046535
10	215.5	13.7	304	6	09BE26
11	215.5	13.7	731	4	P78409
12	213.5	13.6	584	4	000478
13	209.5	13.3	526	4	09HA58
14	208.5	13.2	334	4	09NR44
15	207.5	13.2	319	4	000477
16	207.5	13.2	334	4	09B081
17	207.5	13.2	357	4	015338
18	207.5	13.2	359	4	P78410
19	207.5	13.2	546	4	075658

20	204	13.0	350	4	099420	099420 homo sapien
21	199.5	12.7	290	11	09EP73	09EP73 mus musculus
22	196	12.5	296	13	042404	042404 gallus gall
23	195.5	12.4	275	11	09XR39	09XR39 mus musculus
24	193	12.3	527	4	000475	000475 homo sapien
25	192	12.2	329	6	09XSX6	09XSX6 felis silve
26	192	12.2	332	6	09GM27	09GM27 felis silve
27	189	12.0	586	4	09HCY2	09HCY2 homo sapien
28	188.5	12.0	290	4	09NR07	09NR07 homo sapien
29	186	11.8	529	4	P78408	P78408 homo sapien
30	183	11.6	523	4	000480	000480 homo sapien
31	181	11.5	280	6	09TTF1	09TTF1 canis famill
32	178	11.3	452	11	070355	070355 mus musculus
33	176	11.2	313	11	035531	035531 rattus norv
34	175.5	11.1	455	4	09UR0	09UR0 homo sapien
35	172	10.9	329	6	09TTF2	09TTF2 canis famill
36	171.5	10.9	272	11	070356	070356 mus musculus
37	171.5	10.9	432	4	09Y2C7	09Y2C7 homo sapien
38	169.5	10.8	284	6	09GL33	09GL33 bos taurus
39	168.5	10.7	391	11	035441	035441 mus musculus
40	166	10.5	326	11	070358	070358 mus musculus
41	163	10.4	305	7	09B261	09B261 homo sapien
42	160.5	10.2	325	6	002838	002838 sus scrofa
43	153.5	9.8	325	11	070359	070359 mus musculus
44	152.5	9.7	143	4	09NU62	09NU62 homo sapien
45	151	9.6	339	13	073892	073892 gallus gall

ALIGNMENTS

RESULT 1	
Q9H6B2	PRELIMINARY; PRT; 282 AA.
ID Q9H6B2;	
DT 01-MAR-2001 (TREMBLrel, 16, Created)	
DT 01-MAR-2001 (TREMBLrel, 16, Last sequence update)	
DT 01-JUN-2001 (TREMBLrel, 17, Last annotation update)	
DE CDNA: FLJ22418 FIS, CLONE HRC08590.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX NCBI_TaxId=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,	
RA Ohtani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,	
RA Tanaka T., Nakamura Y., Isegaki T., Sugano S.,	
RT "NDO human CDNA sequencing project."	
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.	
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX	
CC DOMAIN.	
CC EMBL: AK026071; BAB15349.1; -	
DR InterPro: IPR003599; Ig.	
DR InterPro: IPR003600; Ig_Like.	
DR InterPro: IPR003006; Ig_MHC.	
DR Pfam: PF00047; Ig; 1.	
DR SMART: SM00409; Ig; 1.	
DR SMART: SM00410; Ig_Like; 1.	
SO SEQUENCE 282 AA; 30893 MW; 6F9066999A1E9DB4 CRC64;	
Query Match	90.5%; Score 1425; DB 4; Length 282;
Best Local Similarity	99.6%; Pred. No. 4,4e-110;
Matches 281; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY 28 MASIGQILFWISITIIIIIGAILIIIGFISGRHSITVTVAAGNIGEDGILSCFEP 87	
DB 1 MASIGQILFWISITIIIIIGAILIIIGFISGRHSITVTVAAGNIGEDGILSCFEP 60	
QY 88 DIKISDIYIOWLKEGVGLVHEFEKGDSEDEMFGRPTAVADQYVGNASLRKNV 147	
DB 61 DIKISDIYIOWLKEGVGLVHEFEKGDSEDEMFGRPTAVADQYVGNASLRKNV 120	

QY	148	QLAGAGYKCIITISKSGKANLEIKTGASMPENVNDYNASSETLLRCEAPRMEPOPTVY	207
	121	QLTAGAGYKCIITISKSGKANLEIKTGAFSMEPVNDYNASSETLLRCEAPRMEPOPTVY	180
QY	208	WASVDGCANSEVSNTSFELNSENVNMYVSVLYNTINNTYSCTMIENDIAKATGDIKY	267
	181	WASVDGCANSEVSNTSFELNSENVNMYVSVLYNTINNTYSCTMIENDIAKATGDIKY	240
QY	268	TESEIKRRSHQLNLSKASLCVSSFPAISWALLPLSPYIMLK	309
	241	TESEIKRRSHQLNLSKASLCVSSFPAISWALLPLSPYIMLK	282

RESULT	2
Q9BXRL	
ID	Q9BXRL
PRELIMINARY;	PRT; 316 AA.
AC	Q9BXRL;
DT	01-JUN-2001 (Tremblrel. 17, Created)
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE	COSTIMULATORY MOLECULE.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	PubMed=11224528;
RA	Chapoval A.I., Ni J., Lau J.S., Wilcox R.A., Flies D.B., Liu D.,
RA	Dong H., Sica G.L., Zhu G., Tamada K., Chen L.,
RT	"B7-H3: A costimulatory molecule for T cell activation and IFN-gamma
RT	production.";
RL	Nat. Immun. 2:269-274 (2001).
DR	EMBL; AF302102; AAK15438.1; -
SQ	SEQUENCE 316 AA; 33791 MW; FE97007F191CCFA1 CRC64;

Query Match	Score	DB	Length
Similarity	28.5%	Pred. No. 1	6-12
Matches	74	Conservative	46
		Mismatches	106
		Indels	34
		Gaps	10

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QY      IRMERSPPMASIGOLFEWSIIISIIILAGALALJIGGICSRHSITVTVAASGNIGEDG   79
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      LRRRSGPMSG-----YHNGALGLAMFCITGALEVQVPEDDVALVSTDA    46
        2
QY      ILSCF--EPDIKLSDIVIOMLKEGVGLVHEEKGDESEODEMERGRATAFADVIY   137
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      TLCCSFSPESPFSIAQLMLINQIDTKOIVHSPFAEGD---QGSAVANRTALEPDLAQ   102
        47
QY      GNASRLRNVOYLTAGTAKCYIITSKGGANNLEKRGKA-FSMEVAVVDN-----ASSE   191
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      GNASIRLRORVRVADBSGTTC-VSIRDRGSAASVLQVAAAPSKRSMTLEPNKDLPBGDV   161
        103
QY      TLRCEAPRMFPOTPVMAASQVDOCANFSEVSNTSEFELNSENVTKRVYSVLYNYT-INTYT   250
        | | | | | : | : | : | | | | | | | | | | | | | | | | | | |
Db      TITCSSXYGYDEAEVEFW-QDGQGVPPLTGANTTS-QMANEQGLEDVASHVLRVYLGANGTY   218
        162
QY      SCMIENDIAK--ATGDIKVYT   268
        ||| : | : | : | |
Db      SCLVRNPVLOODAGSVTIIT   238
        219
```

RESULT	3	
Q9NM06		
ID	Q9NM06	PRELIMINARY; PRT; 220 AA.
AC	Q9NM06;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, last sequence update)	
DT	01-JUN-2001 (TrEMBLrel. 17, last annotation update)	
DE	CNNA FLJ20685 FIS. CLONE KAI1A3109.	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

OC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
OX NCBI_TaxId:9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=ILEAL MUCOSA.
RA Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
RA Hirao M., Omori Y., Ota T., Suzuki Y., Okeyashi M., Nishi T.,
RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.,
RT "NEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AK006592; BA91323.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00410; Ig_1like; 1.
SO SEQUENCE 220 AA; 24979 MW; 66967620E130B515 CRC64;

	Query March	14.3%	Score 225;	DB 4;	Length 220;
	Best Local Similarity	31.18%	Pred. No. 6.4e-11;		
	Matches 61;	Conservative	32;	Mismatches 81;	Indels 22; Gaps 7;
QY	73 GNIGEDGILSCFEEDILSDIVIOMLKEGVGLVHEFEKEGKDELSEDDEMGRGRAVPA	132			
	: : : : : : : : : : : : : : : : :				
Db	41 GRLEDILTPSFE--RGSEVVIIMKKYQDSY-KVHSYKSGDHLSDPRRANNTSLFY	96			
QY	133 DOYIVGNASLRKANKQLDADGYKCIYITTSKCGKANILEYTGAFSMPEVANDYASSET	192			
	::: : : : : : : : : : : : : : : :				
Db	97 NEIONGNASLPRRVSLLDEGLYTCVGTALOVITNKVYLKAGVELTPMKKEKRNTPSF	156			
QY	193 LRCEAPRPFPOPTVVMASQVDOGA---NFEV-SNFSFELNSEWVTMKVSVLENVN-I	246			
	: : : : : : : : : : : : : : : : : :				
Db	157 LIGSVLSVYPRPIIMW-KMDNTPISENNMEETGSLDPSINSF-----LNIIGS	204			
QY	247 NNTYSCHTENDIAKAT	262			
	: : : : : : : : : : : : : : : : :				
Db	205 NSSECTCTENSLKOT	220			

RESULT	4			
09UM44				
ID	09UM44	PRELIMINARY:	PRT:	414 AA.
AC	Q9UM44;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)			
DE	HERV-H LTR ASSOCIATING PROTEIN 2.			
GN	HHLA2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93375318; PubMed=10444326;			
RA	Mager D. L., Hunter D. G., Schertzer M., Freeman J. D.;			
RT	"Endogenous retroviruses provide the primary polyadenylation signal			
RT	for two new human genes (HHLA2 and HHLA3).";			
RL	Genomics 59:255-263(1999).			
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN.			
DR	EMBL: AF126162; AAD48396.1; -.			
DR	InterPro: IPR003559; Ig.			
DR	InterPro: IPR003600; Ig_like.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; Ig. 2.			
DR	SMART: SM00409; Ig. 2.			
DR	SMART: SM00410; Ig_like. 1.			
DR	SEQUENCE 414 AA; 46850 MW; D645383E1562F70E CRC64;			

RESULT	5	
000481		
ID	000481;	PRELIMINARY;
AC	000481;	PRT: 513 AA.
DT	01-JUL-1997 (Tremblrel. 04, Created)	
DT	01-JUL-1997 (Tremblrel. 04, Last sequence update)	
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)	
DE	BUTYROPHILIN.	
GN	BPE5.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Ruddy D.A., Kronmal G.S., Lee V.K., Mintler G.A., Quintana L.,	
RA	Domínguez R., Meyer N.C., Basava A., McClelland E., Fullan A.,	
RA	Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchihashi Z.,	
RA	Wolff R.K., Schatzman R.C., Feder J.N.;	
RL	Submitted (FEB-1987) to the EMBL/Genbank/DBJ databases.	
CC	1- SIMILARITY: to the IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX	
CC	DOMAIN.	
DR	EMBL; U90552; AAB53430.1; -	
DR	InterPro; IPR001870; Gamma_carboxylase.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003877; SPR.	
DR	Pfam; PF00047; Ig_1.	
DR	Pfam; PF00622; SPRy_1.	
DR	SMART; SM00409; IG_1.	
DR	SMART; SM00449; SPRy_1.	
DR	SeqUence 513 AA; 57762 MW; CD334D7727CD1F63 CRC64;	

OY	235 MKVV--SVLYVVTNNNYSCMIENDIKACGDIVKTESEIKRSHLOLNSAKLCSS-	291
	: : :	: :
Dd	201 LYNAASVIMMGSSGEEVSCTI-----RSSLLGLEKTASTIADP	240
OY	292 FF--AISM-ALLPLPYLM	308
	:	:
Dd	241 FFRSAQRRIALARTLEVLL	261

RESULT	6	
09HCY1		
ID	Q9HCY1	PRELIMINARY; PRT; 513 AA.
AC	Q9HCY1;	
DT	01-MAR-2001 (TREMBLrel, 16, Created)	
DT	01-MAR-2001 (TREMBLrel, 16, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel, 17, Last annotation update)	
DE	D45521.3 (BUTYROPHILIN, SUBFAMILY 3, MEMBER A1).	
GN	BTN3A1.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Phillips S.;	
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.	
CC	1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.	
DR	EMBL: AL021917; CAC03424.1; -.	
DR	InterPro: IPR001870; Gamma_carboxylase.	
DR	InterPro: IPR003559; Ig.	
DR	InterPro: IPR003006; Ig_MHC.	
DR	InterPro: IPR003877; SPRY.	
DR	Pfam: PF00047; Ig_1.	
DR	Pfam: PF006622; SPRY; 1.	
DR	SMART: SM00409; IG_1.	
DR	SMART: SM00449; SPRY; 1.	
DR	SEQUENCE 513 AA; 57677 MW; 80834D70526D16F6 CRC64;	

Query Match	14.2%	Score 223	DB 4	Length 513
Best Local Similarity	26.4%	Pred. No. 3e-10		
Matches	69	Conservative	44	Mismatches 108; Indels 40; Gaps 10;

Query	62	HSITVTTVASAGNI----	GEDGILSCFFEPDIKISLDIVIQMLKRCVGLVHEHREKDEL	117
Db	27	HSAPFSYVGPSPGLLAWGEGDADLPCHLFPEPMSAETMLKVVSSLRQYVVVYADGKEVE	86	
QY	118	SEODEMFGRAVADQIVGNASLRKKNQDITAGTYKCYIITSKGGNNLEKTCAF	177	
Db	87	DROGAPYRGRYSILRDGITACKALRIHNVYASDSGKYLTCFQDGFPEKHALVELKVAAL	146	
QY	178	SMEPVND--YNASSETLRCEAPRPEOPTVYVASOVDGANESEVNTSFEIENSENT	234	
Db	147	G-SPLHDVQKYGKDGIGIHLCRSTGWYPOQIOMSN--NKGEN--IPTVEAPVADSVG	200	
QY	235	MKVY--SYLVNVTINNTYSCHIENDIAKATGDIKTESFIRRSHTQLLNKASLCVSS-	291	
Db	201	LYAAVASVIMRGSSGEGVSCPI-----RSLGLGEXTASTSIADP	240	
QY	292	FF--AISW--ALLPLSPYML	308	
Db	241	FFRSAGRIWIALACTLPVLL	261	

RESULT	7	
ID	Q9H730	
AC	Q9H730	PRELIMINARY; PRT; 347 AA.
DT	01-MAR-2001 (TrEMBLrel. 16, Created)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	
DE	CNA: FLJ21458 F1S, CLONE COL004713.	


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RESULT 10
09BE26 PRELIMINARY; PRT; 304 AA.
ID 09BE26;
AC 09BE26;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOPHYSAL 33.1 KDA PROTEIN.
OC Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxId=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FRONTAL CORTEX;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries." (Apr-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB060220; BAB41154.1; -.
KW Hypothetical protein.
SQ SEQUENCE 304 AA; 33103 MW; 962F3123610AD8A8 CRC64;

Query Match 13.7%; Score 215.5; DB 6; Length 304;
Best Local Similarity 27.4%; Pred. No. 6.1e-10;
Matches 55; Conservative 38; Mismatches 97; Indels 11; Gaps 6;

OY 75 IGEGLSCFTEPDIKLSDIYIOWLKEGVLGIVHEFEKGEKDELSEODEMFGRTAVFADQ 134
Db 44 VGEDADLPCHLFPWMSFETHELMRWSSSLROYVNVADGKEVEDRQSAPIKGRSILRDD 103
OY 135 VIVGNASRLKKNVOLTDACTYCYITTSKGNANLEKTCGAF-SMPEVNV-DYNASSET 192
Db 104 IAGKALRLHNVYASDSGKLYCFQDGFYEKALVELKVALGSLNHLVEKVGEDGIIH 163
OY 193 LRCAPRFPQPTVYVNASQVDOGANSESVTSFELNSENTMKVY--SVLYNTYNTNTY 250
Db 164 LECSTGMYPOPKIOWNSNA--KGONIPAV--EAPVYADGVLAVASVIMRGSGSESV 218
OY 251 SCMIENDI--AKATGDIKYTE 269
Db 219 SCIRNSVLEKTKASTISAD 239

RESULT 11
P78409 PRELIMINARY; PRT; 731 AA.
ID P78409;
AC P78409;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BUTYROPHILIN.
GN BT3.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98044204; Pubmed=9382921;
RA Tazl-Ahmini R., Henry J., Offer C., Bouissou-Bouchouata C.,
RA Mather I.H., Pontarotti P.;
RT "Cloning, localization, and structure of new members of the
RT butyrophilin gene family in the juxta-telomeric region of the major
RT histocompatibility complex."
CC Immunogenetics 47:55-63(1997).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
EMBL: U97502; AAC02656.1; -.

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DR EMBL: U97500; AAC02656.1; JOINED.
DR EMBL: U97501; AAC02656.1; JOINED.
DR EMBL: U90143; AAC02651.1; -.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003877; SPRY.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00622; SPRY; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00449; SPRY; 1.
DR SMART: SM00449; SPRY; 1.
SQ SEQUENCE 731 AA; 81393 MW; 2F0E0A32B73685F0 CRC64;

Query Match 13.7%; Score 215.5; DB 4; Length 731;
Best Local Similarity 25.0%; Pred. No. 2.1e-09;
Matches 62; Conservative 49; Mismatches 110; Indels 27; Gaps 9;

OY 46 LAGAIA-LIIGFISGRHSITVTVASA-----GNIGEDGILSCFTEPDIKLS 92
Db 1 MASSLAFLLNFHVS-LFVOLLTPCSAQSIVLSPGPILLAMVEDADLPCHLFTPSAE 59
OY 93 DIVIOWLKEGVLGIVHEFEKGEKDELSEODEMFGRTAVFADQVTVGNASRLKKNVOLTDA 152
Db 60 TMELRWVSSSLRQYVNVYADGKEVEYRQSAFYRGRTSILRDGITAAGKALRIHNVYASDS 119
OY 153 GTYKCYITTSKGNANLEKTCGAF-SMPEVNV-D--YNASSETLRCEAPRFPQPTVYVNA 209
Db 120 GKLYCYFOHGFYEKAPVELKVALG--SDLIEKVGVDGDIHLECRSTGYVPOQIOWMS 178
OY 210 SQVDOGANSESVTSFELNSENTMKVY--SVLYNTYNTNTYSCMIENDI--AKATGDI 265
Db 179 D--SKENIPAVEG---PVNVYGVGLAVPPVYINTGTSGGVCITINSLGLEKTAISI 233
OY 266 KTESEIK 273
Db 234 SIADPFID 241

RESULT 12
O00478 PRELIMINARY; PRT; 584 AA.
ID O00478;
AC O00478;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BUTYROPHILIN.
GN BT3.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruddy D.A., Krommal G.S., Lee V.K., Mintler G.A., Quintana L.,
RA Domingo R., Meyer N.C., Basava A., McClelland E., Fullan A.,
RA Woff R.K., Schatzman R.C., Feder J.N.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Phillips S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
EMBL: U90548; AAB53426.1; -.
DR EMBL: AL021917; CAA17273.1; -.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003877; SPRY.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00622; SPRY; 1.

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DR SMART: SM00409; IG: 1.
DR SMART: SM00449; SPRY: 1.
SQ SEQUENCE 584 AA; 65001 MW; 2B279B9141E0327F CRC64;

Query Match 13 6%; Score 213.5; DB 4; Length 584;
Best Local Similarity 24.6%; Pred. No. 2.2e-09;
Matches 60; Conservative 50; Mismatches 107; Indels 27; Gaps 9;

QY 46 LAGAAI-LIIFGIGSHSITVTTVASA-----GNIGEDGILCTFEPDILKS 92
DB 3 MASSLAFLLNHFVS-LFVQLLPSCAQSFLGSPSPTILAMGEDADLPCHLFPPTSAE 61

QY 93 DIYIOMLKEGVGLVHEFEKCKDELSEQDEMFRGRTAVFADQYVGNASLRKNVQLTDA 152
DB 62 TMLERWSSSLRQVYVNYADGKEVEDRQSAFYRGRTSILDGITAGKAALRHNVTSDS 121

QY 153 GTKCYIITSKGNANLEKTAFAFMEPVNV-----YNASSELRCAFPWPOPTVMA 209
DB 122 GKLYCFQDDGFYEKALVELKVALG-SDLHIEKGYEDGCIHLECRSTGWYPOQIKWS 180

QY 210 SQVDGAFSEVNTSPFELSENVTMKV--SVLYNTVINTYSCMIENDI--AKAGDI 265
DB 181 D--TKGNIRPV---EAPVYADGVGLYAAVYIMRSGSGVSCIIRNSLLEKTAFT 235

QY 266 KYTE 269
DB 236 SIAD 239

RESULT 13
ID 09H458 PRELIMINARY; PRT; 526 AA.

AC 09H458; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BK1489.2 (BUTYROPHILIN, SUBFAMILY 1, MEMBER A1).

GN BTN1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

CC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tracey A.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR EMBL: AL121936; CAC16802.1; -.
DR InterPro: IPR001870; Gamma_carboxylase.

DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR InterPro: IPR003877; SPRY.

DR Pfam: PF00047; Ig_1.
DR Pfam: PF00622; SPRY_1.
DR SMART: SM00409; IG_1.
DR SMART: SM00406; IGV_1.
DR SMART: SM00410; IG_Like_1.
DR SMART: SM00449; SPRY_1.

SQ SEQUENCE 526 AA; 58960 MW; 4585D5CE88A2ECA4 CRC64;
Query Match 13.3%; Score 209.5; DB 4; Length 526;
Best Local Similarity 26.6%; Pred. No. 4.1e-09;
Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;

QY 75 IGEDGILCTFEPDILKSDIVIOMLKEGVGLVHEFEKCKDELSEQDEMFRGRTAVFADQ 134
DB 42 VGEDADLPCHLFPPTSAEELMELKVAWSSSLRQVYVNYADGKEVEDRQSAFYRGRTSILRPG 101

QY 135 VIVGNASLRKNVQLTDAGTYKCYIITSKGNANLEKTAFAFMEPVNVYNASSE-T 192
DB 102 IAKGRVALRIKRVAVSDGETCTCFREDGSEELVHLKVAALGSDPHISMQOENGEIC 161
QY 193 LRCEAPRWPOPTVMAVQVDGAFSEVNTSPFELSENVTMKVSVLYNTVINTYSC 252
DB 162 LECRSVGMWPEPQVQW--RTSKGKFPSTSE-SNPDEGLFTVMAVSIIRDSAKNVSC 218

QY 253 MIEN 256
DB 219 YIQN 222

RESULT 14
ID 09NR44 PRELIMINARY; PRT; 334 AA.

AC 09NR44; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BUTYROPHILIN, SUBFAMILY 3, MEMBER A2.

GN BTN3A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

CC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes D.A., Stammers M., Malcherek G., Beck S., Trowsdale J.;
RT "Genomic structure of the btf (butyrophilin-like) gene cluster on human chromosome 6."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

CC -1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR EMBL: AF257505; AAF6140.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00409; IG_1.

SQ SEQUENCE 334 AA; 36399 MW; 95CFE887DB0DBAE4 CRC64;
Query Match 13.2%; Score 208.5; DB 4; Length 334;
Best Local Similarity 26.1%; Pred. No. 2.7e-09;
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

QY 75 IGEDGILCTFEPDILKSDIVIOMLKEGVGLVHEFEKCKDELSEQDEMFRGRTAVFADQ 134
DB 44 VGEDADLPCHLFPPTSAEELMELKVAWSSSLRQVYVNYADGKEVEDRQSAFYRGRTSILRPG 103

QY 135 VIVGNASLRKNVQLTDAGTYKCYIITSKGNANLEKTAFAFMEPVNV-DYNASSET 192
DB 104 ITAGKAAALRIHNVTSADSGKYLCDGFYEKALVELKVALGSLHVEVKGEDGTH 163

QY 193 LRCEAPRWPOPTVMAVQVDGAFSEVNTSPFELSENVTMKVSVLYNTVINTYSC 252
DB 164 LECRSVGMWPEPQVQW--RTSKGKFPSTSE-SNPDEGLFTVMAVSIIRDSAKNVSC 218

QY 241 LYNTVINTYSCMIENDI--AKATGDIKYTE 269
DB 209 IMKSGSGEGVSCIIRNSLLEKTAFTSISAD 239

RESULT 15
ID 000477 PRELIMINARY; PRT; 319 AA.

AC 000477; 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BUTYROPHILIN.
GN BTF4.
OS Homo sapiens (Human).

OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
 OC Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ruddy D.A., Kronmal G.S., Lee V.K., Mintier G.A., Quintana L.,
 RA Domingo R., Meyer N.C., Basava A., McClelland E., Fullan A.,
 RA Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchihashi Z.,
 RA Wolff R.K., Schatzman R.C., Feder J.N.;
 RL Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: U90546; AAB53424.1; .
 DR InterPro: IPR003599; Ig_
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00409; Ig; 1.
 SQ SEQUENCE 319 AA; 34734 MW; 1697EF524F558749 CRC64;

Query Match 13.2%; Score 207.5; DB 4; Length 319;
 Best Local Similarity 26.1%; Pred. No. 3e-09;
 Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;
 QY 75 IGEDGILSCTEFPEPDIKLSDIVIOMLKEGVGLVHEFEKDELSQDEMFGRGTAVFADQ 134
 Db 44 VGEDADLPCHLPFPMASATMELKVVSSSLROYVNVYADGKEYEDRQSAFYRGRTSILRDG 103
 QY 135 VIVGNASIRLKNVQLTDAGTYKCYLITTSKGNANLEKYGAF-SMPEVNV-DYNASSET 192
 Db 104 ITAGKAALRIHNVTASDSGKTYCFQDGDFFEKALVELKVAALGSNLHVEYKGYEDGCIH 163
 QY 193 LRCAFRWFEPOPTVWV-----ASVDGAGNFSEVSNTSFLENSENTMKVYVSV 240
 Db 164 LECRSTGWYPOPOIQWSNAKGENIPAVEAPYVADGVGLYEVA-----ASV 208
 QY 241 LYNTYINTYSCMIENDI--AKATGDIKYTE 269
 Db 209 IMRGSGRGVSCITRNSLGLKTRASISIA 239

Search completed: February 15, 2002, 14:23:16
 Job time: 206 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 15, 2002, 14:18:55 ; Search time 16.06 Seconds

(Without alignments)
1465.625 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574

Sequence: 1 HASAHASGRQLHSASNTQI.....SSFAISWALLPLSPYLMK 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219.5	13.9	526	2	butyrophilin - boy
2	211.5	13.4	526	2	butyrophilin - boy
3	171.5	10.9	487	2	butyrophilin - mou
4	168.5	10.7	391	2	butyrophilin homol
5	163.5	10.4	299	2	CD80 precursor - r
6	151	9.6	339	2	Ig V-region-like B
7	150.5	9.6	340	2	Ig V-region-like B
8	150	9.5	247	2	myelin/oligodendro
9	147.5	9.4	329	1	B7-2 antigen - hum
10	147.5	9.4	330	2	CD86 precursor - r
11	147	9.3	218	2	myelin/oligodendro
12	146.5	9.3	372	2	Ig V-region-like B
13	146	9.3	398	2	Ig V-region-like B
14	144	9.1	247	2	myelin/oligodendro
15	143.5	8.9	246	2	gene B7-2 protein
16	140.5	8.6	761	1	neural cell adhesi
17	135	8.5	503	2	SHP substrate-1 pr
18	134.5	8.5	503	2	neural cell adhesi
19	133	8.4	1091	1	neural cell adhesi
20	132.5	8.4	853	1	neural cell adhesi
21	130.5	8.3	725	1	neural cell adhesi
22	130.5	8.3	1033	2	cell adhesion mole
23	130.5	8.3	1115	1	neural cell adhesi
24	128.5	8.2	858	1	neural cell adhesi
25	127	8.1	946	1	for-related recept
26	126.5	8.0	765	2	cell adhesion mole
27	126.5	8.0	812	2	cell adhesion mole
28	126.5	8.0	932	2	cell adhesion mole
29	126.5	8.0	1088	1	neural cell adhesi

30	125.5	8.0	1018	2	JC4211	neural adhesion pr
31	124	7.9	309	2	I49503	B-lymphocyte activ
32	123.5	7.8	725	2	JE0099	neural cell adhesi
33	123.5	7.8	5175	2	T20992	hypothetical prote
34	123.5	7.8	5198	2	T43290	hemikentlin precurs
35	122.5	7.8	871	1	I48696	protein-tyrosine k
36	122.5	7.8	881	1	I48697	protein-tyrosine k
37	121.5	7.7	1612	2	T30805	dufil protein - mo
38	121	7.7	321	2	I54766	B-lymphocyte activ
39	121	7.7	1091	2	S01998	contactin precurs
40	120	7.6	215	2	A57843	sodium channel bet
41	120	7.6	288	2	A45803	B-cell-restricted
42	120	7.6	333	2	A31923	amalgam protein pr
43	118	7.5	321	2	D39371	Ig V-region-like B
44	118	7.5	423	2	T29549	hypothetical prote
45	117.5	7.5	725	2	JE0100	neural cell adhesi

ALIGNMENTS

RESULT 1
A37821
butyrophilin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
R:Accession: A37821
R:Jack, L.J.W.; Mather, I.H.
J. Biol. Chem. 265, 14481-14486, 1990
A:Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein

A:Reference number: A37821; MUID:90354441
A:Accession: A37821
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-526 <JAC>
A:Cross-references: GR:M35551; NID:q1763685; PIDN:AAB39766.1; PID:q162773
C:Keywords: transmembrane protein

Query Match 13.9%; Score 219.5; DB 2; Length 526;
Best Local Similarity 25.0%; Pred. No. 3.4e-09;
Matches 49; Conservative 48; Mismatches 94; Indels 5; Gaps 4;

QY 75 IGEGLITSCFFEPPIKSDIVIQWLKGCYGLVHEFEKDELSQDPMFRGTAVRADQ 134
Db 42 VGEPAELPCRLSPVSAKGMELRMFRKVPSPAVSREGEQEEAAYRGVSLVEDH 101
QY 135 VIVGNASLRKKNVQUTDAGTYKCYIIRSKGKGNANLEKKGAF-SMPEVNVYDVAASPE-T 192
Db 102 IAEBSVAVRIOEVKASDDGETCFRRDENTEERAIYHLKVAALGSDPHISKVQESGEIQ 161
QY 193 LRCEAPRFPOPTVMAASQVDGAFSEVNTSPFELNSENVTMKVSLVYVNTINTYSC 252
Db 162 LECISVGMWPEPQVQW--RFRGGEFPMSSSRNPDEGLTTVAASVILIRSSKNV-SC 218
QY 253 MIENDIAKATGDIKVT 268
Db 219 CIRMLLGOEKDVEVS 234

RESULT 2
S70587
butyrophilin precursor - human
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
R:Accession: S70587
R:Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.
Bloodm. Biophys. Acta 1306, 1-4, 1996
A:Title: Cloning and sequence analysis of human butyrophilin reveals a potential role in cell adhesion
A:Reference number: S70587; MUID:96201696
A:Accession: S70587
A>Status: preliminary

R. Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Submitted to the EMBL Data Library, October 1997

QY 206 VVMSQVDQGANSEVSNSTFELNSENVTKRVSVL-VNVTINNYSCTMIENDIAKATGD 264
: | : : | | : : : | | : | | : : : | :
Db 172 LAM---MEDGEELNAV-NTVVDQDDLTLELYSVSSELDNVTNNHSIVCLIK-----YGE 221

QY 265 IKYTE---SEIKRRSHLOLNSKASLCVSSFFAISWALLDLSPLYML 308
 Db 222 LVSQIFPWSKROEPPIDLP-----FWIIRVSGALVL 256

RESULT 6

T28138
 Ig V-region-like B-G antigen, isoform 2 - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C/Accession: T28138
 R/Milne, S.; Kaufman, J.; Beck, S.
 submitted to the EMBL Data Library, May 1998
 A/Description: DNA sequencing and analysis of the chicken major histocompatibility comp
 A/Reference number: 220475
 A/Accession: T28138
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-339 <MIL>
 A/Cross-references: EMBL:AL023516; PIDN:CAA18959.1
 A/Experimental source: clone CB12
 C/Genetics:
 A/Gene: B-G 2
 A/Map position: 16
 A/Introns: 34/1; 148/1; 183/1; 189/1; 196/1; 203/1; 210/1; 217/1; 224/1; 231/1; 239/1; 2

Query Match 9.6%; Score 151; DB 2; Length 339;
 Best Local Similarity 21.7%; Pred. No. 0.00034;

Matches 56; Conservative 46; Mismatches 90; Indels 66; Gaps 10;

QY 63 SITVTVASAGNIGEDGILCTFEP--DIKLSDIYQWLKRGVGLVHEFEKGDSEQ 120
 Db 42 SLRYTAI-----VGDVVLRCOLSPCKDAMSSD--IRWIOHRTSGFVHHYONGED--LEQ 92
 QY 121 DEMFRGRTAVFADQYIVGNASLRKKNQVLTGAGTKYKCIITISKGGANLEKTCAGFEMP 180
 Db 93 MEETKGRTELRLKGLSDGNLDLRITAVSTSDSGSCAVLDGDDGADA----- 140
 QY 181 EVNVYNASSETLRCEAPRMFPPOPTVW-----ASQVDOG 215
 Db 141 --VVDLEVSDP-----FSQITHPKVAVLAVITLVGSFVITVFLYRKKAETTKOK 189
 QY 216 ANFESEVNTSELSN-----ENVTMKVSVLYNVTINNT--YSCMIENDIAKATGDI-KVT 268
 Db 190 GKDELEEMDAKGLTLAELERDPAKLETLVENLERNTFERAKKLASELERRNQDLKLA 249
 QY 269 ESEIKRRSHLOLNSKAS 286
 Db 250 SDLVQOTKRAVEKLSQWS 267

RESULT 7

T28137
 Ig V-region-like B-G antigen, isoform 1 - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C/Accession: T28137
 R/Milne, S.; Kaufman, J.; Beck, S.
 submitted to the EMBL Data Library, May 1998
 A/Description: DNA sequencing and analysis of the chicken major histocompatibility comp
 A/Reference number: 220475
 A/Accession: T28137
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-340 <MIL>
 A/Cross-references: EMBL:AL023516; PIDN:CAA18958.1
 A/Experimental source: clone CB12
 C/Genetics:
 A/Gene: B-G 2
 A/Map position: 16
 A/Introns: 34/1; 148/1; 183/1; 190/1; 197/1; 204/1; 211/1; 218/1; 225/1; 232/1; 240/1; 2

Query Match 9.6%; Score 150.5; DB 2; Length 340;
 Best Local Similarity 32.4%; Pred. No. 0.00037;
 Matches 35; Conservative 22; Mismatches 40; Indels 11; Gaps 4;

QY 63 SITVTVASAGNIGEDGILCTFEP--DIKLSDIYQWLKRGVGLVHEFEKGDSEQ 120
 Db 42 SLRYTAI-----VGDVVLRCOLSPCKDAMSSD--IRWIOHRTSGFVHHYONGED--LEQ 92
 QY 121 DEMFRGRTAVFADQYIVGNASLRKKNQVLTGAGTKYKCIITISKGGANLEKTCAGFEMP 180
 Db 93 MEETKGRTELRLKGLSDGNLDLRITAVSTSDSGSCAVLDGDDGADA 140

RESULT 8

A55717
 myelin/oligodendrocyte glycoprotein precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 08-Oct-1999
 C/Accession: A55717; C47712
 R/Daubas, P.; Pham-Dinh, D.; Dautigny, A.
 Genomics 23, 36-41, 1994
 A/Title: Structure and polymorphism of the mouse myelin/oligodendrocyte glycoprotein
 A/Reference number: A55717; MUID:95130110
 A/Accession: A55717
 A/Molecule type: DNA
 A/Residues: 1-247 <DAU>
 A/Cross-references: GB:I29498
 R/Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Rousset, G.; Pontarotti, P.; Roedel
 Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993
 A/Title: Myelin/oligodendrocyte glycoprotein is a member of a subset of the Immunog
 A/Reference number: A47712; MUID:93376728
 A/Accession: C47712
 A/Molecule type: mRNA
 A/Residues: 30-95, 'E', 97-247 <PHA>
 A/Cross-references: GB:I20942; NID:g393588; PIDN:AAA03180.1; PID:g393589
 C/Genetics:
 A/Gene: MOG
 A/Map position: 17
 A/Note: encoded within the MHC
 C/Function:
 A/Description: may be involved in lipid interaction; may be involved in cell-cell c
 C/Keywords: glycoprotein; myelin; transmembrane protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-247/Product: myelin/oligodendrocyte glycoprotein #status predicted <MAT>
 F:151-119/Domain: transmembrane #status predicted <TM>
 F:204-229/Domain: transmembrane #status predicted <TM>
 F:60/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 9.5%; Score 150; DB 2; Length 247;
 Best Local Similarity 23.8%; Pred. No. 0.00027;

Matches 34; Conservative 33; Mismatches 66; Indels 10; Gaps 2;

QY 37 WS-----ISIIILAGALILIGFISGRHSITVTVASAGNIGEDGILCTFEPDIR 90
 Db 5 WFSWSPSCFLSLLL-----LLQSCSYAGFRTIGPEYIRALVGDPAELPCRLSPGKN 60
 QY 91 LSDIYQWLKRGVGLVHEFEKGDSEQDEMFRGRTAVFADQYIVGNASLRKKNQVLT 150
 Db 61 ATGHEVGVYRSPFSRVVLLYLNKGDDQAPERYGRTELKELTISEGKVLRIQNVFS 120
 QY 151 DAGTYKCYIISKGGANLEK 173
 Db 121 DEGGTCFFRDHSYQEEAMELK 143

RESULT 9

A48754
 B7-2 antigen - human
 N/Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
 C/Species: Homo sapiens (hmn)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

Fri Feb 15 14:25:10 2002

us-09-636-801-392.rpr

Page 6

A:Accession: I49522
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-309 <RSS>
A:Cross-references: GB:L25606; NID:g432478; PIDN:AA79770.1; PID:g432479
C:Genetics:
A:Gene: B7-2
C:Superfamily: B7-2 antigen

Query Match	9.1%	Score 14.3	DB 2	Length 309
Best Local Similarity	22.6%	Pred. No. 0.0011		
Matches 50	Conservative 53	Mismatches 83	Indels 35	Gaps 10

```

QY      64  ITVTVAASAGI-----GEGDILSCF--EPDILSDIYOMLKEBVLIGHNEFKRGD 115
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      15  VTVLLISAVSVEIQANFNGATATLPCEPFTKQNSISELSEVFMODQOL--VLEHHYIGTE 73

QY      116  ELSODEMFNGRTAVFADQVITGNASLRKKNVOLTDSATKCYLITTSKRGKANLEK-- 173
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      74  KLDVNAKYLGRTSF--DR--NMWTLRLHNHYQIKDMSGVDCFTQKKRPPGSIITLQOTLT 128

QY      174  ----TGAFSMEVANDVNASSET---LRCEAPRMFPOPTVYVMAQVDQGANFSEVSNTSF 226
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      129  ELSVIANESEPEIKLAONVNGSINGLITCTSKOCHPRKRMKMYELITNSTNEYGD---NM 184

QY      227  ELNSENVTMKVVSIVYNTI-----NNYVSCMIENDIAK 260
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      185  QISODNNT-ELFSTISNLSLSPFGVGHMHTVVCVLETESMK 224

```

Search completed: February 15, 2002, 14:20:40
Job time: 105 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 15, 2002, 14:20:20 ; Search time 9.96 Seconds

(without alignments)
1137.493 Million cell updates/sec

Title: US-09-636-801-392
Perfect score: 1574
Sequence: 1 HASAHASGRQLHSASTQI.....SSFFAISMALPLSPYLMK 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215.5	13.7	526	1 BUTY_BOVIN	P18892 Bos taurus
2	211.5	13.4	526	1 BUTY_HUMAN	Q13410 homo sapien
3	178.5	11.3	524	1 BUTY_MOUSE	O62556 mus musculu
4	163.5	10.4	299	1 CD80_RABIT	P42070 coryctolagus
5	152	9.7	245	1 MOG_RAT	O63345 rattus norv
6	150.5	9.6	246	1 MOG_MOUSE	O61883 mus musculu
7	147.5	9.4	302	1 ICOL_HUMAN	O75144 homo sapien
8	147.5	9.4	329	1 CD86_HUMAN	P42081 homo sapien
9	147.5	9.4	330	1 CD86_RABIT	P42071 coryctolagus
10	144	9.1	247	1 MOG_HUMAN	O16653 homo sapien
11	143.5	9.1	309	1 CD86_MOUSE	P42082 mus musculu
12	140.5	8.9	246	1 MOG_BOVIN	P58033 bos taurus
13	135	8.6	761	1 NCAL_HUMAN	P13592 homo sapien
14	135	8.6	848	1 NCAL_HUMAN	P13591 homo sapien
15	132.5	8.4	853	1 NCAL_BOVIN	P18363 bos taurus
16	131	8.3	1091	1 NCAL_CHICK	P13590 gallus gall
17	130.5	8.3	725	1 NCAL_MOUSE	P13594 mus musculu
18	130.5	8.3	1115	1 NCAL_MOUSE	P13593 mus musculu
19	128.5	8.2	858	1 NCAL_RAT	P13596 rattus norv
20	126.5	8.0	1088	1 NCAL_MOUSE	P16170 xenopus lae
21	125.5	8.0	298	1 NCAL_HUMAN	P57087 homo sapien
22	124	7.9	306	1 CD80_MOUSE	O00609 mus musculu
23	123	7.8	365	1 CD80_MOUSE	P97789 mus musculu
24	121	7.7	1010	1 CONT_MOUSE	P14781 rattus gall
25	120	7.6	215	1 CIB2_RAT	P54900 rattus norv
26	120	7.6	288	1 CIB2_MOUSE	P54900 rattus norv
27	120	7.6	333	1 AMAL_DROME	P13681 homo sapien
28	120	7.6	365	1 NCAL_HUMAN	P13564 drosophila
29	119	7.6	323	1 NCAL_HUMAN	P18310 homo sapien
30	115.5	7.3	1092	1 NCAL_MOUSE	O18066 caenorhadi
31	114.5	7.3	322	1 NCAL_MOUSE	P36333 xenopus lae
32	113.5	7.2	1336	1 NCAL_MOUSE	O91h18 mus musculu
33	113.5	7.2	1461	1 NCAL_MOUSE	P53767 rattus norv
					Q92859 homo sapien

34	113	7.2	359	1 LACH_DROME	Q24372 drosophila
35	112.5	7.1	337	1 G55A_CHICK	O98892 gallus gall
36	112.5	7.1	1018	1 CONT_HUMAN	O12860 homo sapien
37	112.5	7.1	1020	1 CONT_MOUSE	P12960 mus musculu
38	110	7.0	1036	1 AXOL_CHICK	P28685 gallus gall
39	109.5	7.0	1377	1 NCAL_RAT	P97603 rattus norv
40	107.5	6.8	351	1 CD2_HUMAN	O67729 homo sapien
41	106.5	6.8	347	1 CD2_MOUSE	P37938 equus caball
42	106.5	6.8	413	1 HEMO_MOUSE	P13398 manduca sex
43	106.5	6.8	1338	1 NCAL_HUMAN	P17948 homo sapien
44	106.5	6.8	1447	1 DCC_MOUSE	P70211 mus musculu
45	106	6.7	837	1 NCAL_MOUSE	O35136 mus musculu

ALIGNMENTS

RESULT 1
BUTY_BOVIN STANDARD: PRT: 526 AA.
AC P18892: 018955: 018959:
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BUTYROPHILIN PRECURSOR (BT).
GN BTNL1 OR BTN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX MEDLINE=9035441; PubMed=2387867;
RA Jack L.J.W., Mather I.H.;
RT "Cloning and analysis of cDNA encoding bovine butyrophilin, an apical
glycoprotein expressed in mammary tissue and secreted in association
with the milk-fat globule membrane during lactation.";
RT J. Biol. Chem. 265:14481-14486(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=HOLSTEIN-FRIESIAN;
RA Davey H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V.,
Mather I.H., Wilkins R.J.;
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RA Seyfert H., Luethen F.;
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=9529316; PubMed=7775382;
RA Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.;
RT "Site-specific glycosylation of bovine butyrophilin.";
RT J. Biochem. 117:147-157(1995).
CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
MEMBRANE.
CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
(BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
CC -!- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY. CONTAINS 1
V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
CC -!- SIMILARITY: STRONG. TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).
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MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA MEMBRANE (BY SIMILARITY).

- I SUBUNIT : SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE (BY SIMILARITY).

- I SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- I SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 1 V-LIKE DOMAIN. BELONGS TO THE BTM/MOG SUBFAMILY.

- I SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).-----

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CC EMBL; U09576; AAC50489.1; -.
CC MIM; 601610; -.
DR InterPro: IPR003879; Butyroph. DUF.C.
DR InterPro: IPR001870; Gamma_catbxyIse.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_LV.
DR InterPro: IPR003877; SPRY.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00622; SPRY; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00449; SPRY; 1.
KM Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 526 BUTYROPHILIN.
FT DOMAIN 27 526 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 243 269 POTENTIAL.
FT DOMAIN 270 526 CYTOPLASMIC (POTENTIAL).
FT CAROHRD 55 55 N-LINKED (GLCNAG. .) (POTENTIAL).
FT CAROHRD 215 215 N-LINKED (GLCNAG. .) (POTENTIAL).
SQ SEQUENCE 526 AA; 59004 MW; E9EACAFBDAR94d5 CRC64;

Query Match 13.4%; Score 211.5; DB 1; Length 526;
Best Local Similarity 26.6%; Pred. No. 7.2e-10;
Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;

OY 75 IGEDDILSCTFEPDKLSDIVIOMLKBEVLGIYHFKEKGKDELSSDDMFGRGRTAVFDQ 134
DB 42 VGDEDELFCRLSPNNSAEHLIRMKRVPAVLVYHRRGRDEAQMPEYGRATLVODG 101
OY 135 VIVGNASLRKLNVQLTDAGTYKYCIITSKSGKANLEVKGAFL-SMPEVNVDYNASSE-T 192
DB 102 IAKGRAVALRINGVRVSDSGEYTCFPEREGSGYEALVHLKVALGSDPHISMVGENGSLC 161
OY 193 LRCEAPRFPPPTVYVASQVDGANGSESVNTSELNSENVTMYKVSYLVNTVINTNYSC 252
DB 162 LECTSVGVYPEPOVYM-RTSKGKFFSTSE-SRPNDPEGELFTVAASYIIDRTSTKNVC 218
OY 253 MIEN 256
DB 219 YIQN 222

RESULT 3
BUTY_MOUSE STANDARD: PRT; 524 AA.
AC 062556; P97392;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BUTYROPHILIN PRECURSOR (BT).
CN BTM1A OR BTM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurimorphi; Muridae; Eutelesom; Mus

Query Match	11.3%	Score 178.5	DB 1	Length 524
Best Local Similarity	22.7%	Precl. No. 3.6e-07		
Matches	45	Conservative 51	Mismatches 93	Indels 9
				Gaps 4
OY	75	IGEBGLISCTPEPDILKSLDIYIOMLKEBVLGIVHEFEKRGDELSRQDDEMRGRATVAFADQ	134	
DB	43	VGSDBELTCGFSPPASNSSEYMEILFRQTRSTAVLLYRGQGRQGMTEYGRATLATAG	102	
OY	135	VIVGNASILRLNVOLTDAGTYKCYLITTSKGGKGNALYEYKGAFL-SMEPVNVDYNASSE-T	192	
DB	103	LIDGATLILINDIVRSDGGEYRCLEKONDDEEAAVYLKVAAYGSDPQISMTVGENSGME	162	
OY	193	LRCAPRWFPOPTVYVWASQVDGANGFSEVSNT--SEFLNSENVTKVYSLVLYNTINNTY	250	
DB	163	LECTSSGMYPEPOVQWMT-----GNREMLPSTSESKKHNEGLFTVAVSMIRDSISKNM	217	
OY	251	SCMIENDIAKATNGDKVY	268	
DB	218	SCCIQNIILGGQKEVEIS	235	
RESULT	4			
CD80_RABIT				
ID	CD80_RABIT	STANDARD:	PRT:	299 AA.
AC	P42070			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	T LYMHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1 ANTIGEN).			
GN	CD80.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=B/J X CHB;HM;			
RX	MEDLINE=95369849; PubMed=7642234;			
RA	Isono T., Seto A.;			
RT	"Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules."			
RL	Immunogenetics 42:217-220(1995).			
CC	-1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.			
CC	-----			
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CC	-----			
DR	EMBL; D49843; BAA0643.1; -			
DR	InterPro; IPR003599; I9.			
DR	InterPro; IPR003006; I9_MHC.			
DR	InterPro; IPR003600; I9_1like.			
DR	Pfam; PF00047; I9; 1.			
DR	SMART; SM00409; I9; 1.			
DR	SMART; SM00410; I9_1like; 1.			
DR	Immunoglobulin domain; T-cell; glycoprotein; signal; Transmembrane; Receptor.			
KW	SIGNAL			
FT	CHAIN	1	32	POTENTIAL.
FT	DOMAIN	33	299	T LYMHOCYTE ACTIVATION ANTIGEN CD80.
FT	DOMAIN	33	243	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	244	264	POTENTIAL.
FT	DOMAIN	265	299	CYTOPLASMIC (POTENTIAL).

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FT DOMAIN 42 122 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 154 222 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 49 115 POTENTIAL.
FT DISULFID 161 215 POTENTIAL.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 299 AA: 33513 MW: 67442235C091DE0 CRC64;

Query Match 10.4%; Score 163.5; DB 1; Length 299;
Best Local Similarity 25.3%; Pred. No. 2.9e-06;
Matches 73; Conservative 57; Mismatches 89; Indels 69; Gaps 19;

QY 40 ISIIILAGAILIGFISGRHSITVTVAAGNIGEDGILSCFEPDIT-KLSDIYIOW 98
DB 19 LCLLLALAG---LHFSSGIS-----QVTK-----SYKEMALSCDYNISIDELARKHITW 65
QY 99 LKEG--VLGLVHEKKEKDELSEQDEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYK 156
DB 66 QKDOQWLSIIT---SGQVEYVME---YKNRT--FPD--LIINLSLITLRLSDKGTYT 114
QY 157 CYIITSKGNANLEKTKGA-----FSMPEV-----NDYNASSEFLRCEAPRMFPQPT 205
DB 115 C-VVQKQENKSGFRREHLTSTVLSIRADFPVPSITDIGHDPNV--KRIRCSAGSGPEPR 171
QY 206 VVWASOVDOGANFSEVNTSFEIENSENVTKVYVSVL-YNTTINTNTSCMENDIANATGD 264
DB 172 LAM---MEDGELNANV-NITVDODLDELAYSSELDENVTNNHSIVCLIK-----YGE 221
QY 265 IKVTE---SEIKRSHLDLINSKASLGVSSFPFISWALLPLSPYIML 308
DB 222 LVSQIFPMSKPKQEPPIQLP-----FWIIPVSGALVL 256

RESULT 5
MOG_RAT 5
ID MOG_RAT STANDARD; PRT; 245 AA.
AC 063345;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
GN MOG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxId=10116;
RX (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93085763; PubMed=1453482;
RA Gardiner M.V., Amliquet P., Lillington C., Mathieu J.-M.;
RT "Myelin/oligodendrocyte glycoprotein is a unique member of the
RT immunoglobulin superfamily."
RL J. Neurosci. Res. 33:177-187(1992).
RN (2)
RP SEQUENCE OF 28-245 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93376728; PubMed=8367453;
RA Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Rousset G.,
RA Fontarot P., Roeckel N., Mather I.H., Artzt K., Lindahl K.F.,
RA Dautigny A.;
RT "Myelin/oligodendrocyte glycoprotein is a member of a subset of the
RT immunoglobulin superfamily encoded within the major
RT histocompatibility complex."
RL Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
RN (3)
RP STRUCTURE BY NMR OF 62-82.
RX MEDLINE=97354172; PubMed=9210466;

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RA Albouze-Abo S., Wilson J.C., Bernard C.C.A., von Itzstein M.;
RT "A conformational study of the human and rat encephalitogenic myelin
RT oligodendrocyte glycoprotein peptides 35-55."
RL Eur. J. Biochem. 246:59-70(1997).
DB -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
DB COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
DB CELL COMMUNICATION.
DB -1- SUBUNIT: MAY FORM HOMODIMERS.
DB -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DB -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
DB LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
DB MEMBRANES.
DB -1- DEVELOPMENTAL STAGE: A PEAK OF EXPRESSION HAS BEEN OBSERVED
DB BETWEEN POSTNATAL DAYS 15 AND 25, COINCIDENT WITH THE PERIOD OF
DB ACTIVE MYELINATION.
DB -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
DB ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
DB -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)
DB WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
DB -----
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DB or send an email to license@isb-sdb.ch).
DB -----
DB EMBL: M99485; AAA41628.1; -
DB DR EMBL: L21995; AAF74766.1; -
DB DR InterPro: IPR003006; Ig_MHC.
DB DR InterPro: IPR003596; Ig_V.
DB DR Pfam: PF00047; IgV; 1.
DB DR SMART: SM00406; IgV; 1.
DB KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
DB FT SIGNAL 1 27
DB FT CHAIN 28 245 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
DB FT DOMAIN 28 155 EXTRACELLULAR (POTENTIAL).
DB FT TRANSMEM 156 176 POTENTIAL.
DB FT DOMAIN 177 208 CYTOPLASMIC (POTENTIAL).
DB FT TRANSMEM 209 229 POTENTIAL.
DB FT DOMAIN 230 245 EXTRACELLULAR (POTENTIAL).
DB FT DOMAIN 44 132 IG-LIKE V-TYPE DOMAIN.
DB FT DISULFID 51 125 POTENTIAL.
DB FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 245 AA: 27881 MW: C97F8AD06D6A32B4 CRC64;

Query Match 9.7%; Score 152; DB 1; Length 245;
Best Local Similarity 26.2%; Pred. No. 1.9e-05;
Matches 39; Conservative 31; Mismatches 55; Indels 24; Gaps 5;

QY 37 WS-----IISIIIL-----AGAILIIGFISGRHSITVTVAAGNIGEDGILSCT 84
DB 5 WSLSLPSCLSLILLQLQLSRYAGQR-VIGPG-----HPIRL-----VGEALPLPR 52
QY 85 FEPDIKLSIVLIQWLKEGVGLVHEKKEKDELSEQDEMFRGRTAVFADQVIVGNASLR 144
DB 53 ISPGKNATGMEVGMVRSRNVHLRYNGDQAEQAPRYGRTFLKESIGGKVALRI 112
QY 145 KNVQLDAGTYKCYITTSKGNANLEK 173
DB 113 QNVFSDGGYTCFPRDHSYQEEAAVELK 141

RESULT 6
MOG_MOUSE 6
ID MOG_MOUSE STANDARD; PRT; 246 AA.
AC 061885; Q62003; P70364;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.

```


GN MOG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=95130110; PubMed=7829100;
 RA Dabbs P., Pham-Dinh D., Dautigny A.;
 RT "Structure and polymorphism of the mouse myelin/oligodendrocyte
 RT glycoprotein gene.";
 RL Genomics 23:36-41(1994).
 RN 12)
 RP SEQUENCE FROM N.A.
 RA Gardiner M.V., Mathieu J.M.;
 RT "Murine and human MOG are highly conserved: cDNA analysis.";
 RL Trans. Am. Soc. Neurochem. 24:234-234(1993).
 RN 13)
 RP SEQUENCE OF 29-246 FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=93376728; PubMed=8367453;
 RA Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Rousset G.,
 RA Pontarotti P., Roessel N., Mather I.H., Artzt K., Lindahl K.F.,
 RA Dautigny A.;
 RT "Myelin/oligodendrocyte glycoprotein is a member of the
 RT immunoglobulin superfamily encoded within the major
 RT histocompatibility complex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
 RN (4)
 RP SEQUENCE OF 29-54.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=92218912; PubMed=1373175;
 RA Amiguet P., Gardiner M.V., Zanetta J.-P., Mathieu J.-M.;
 RT "Purification and partial structural and functional characterization
 RT of mouse myelin/oligodendrocyte glycoprotein.";
 RL J. Neurochem. 58:1676-1682(1992).
 CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
 CC COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
 CC CELL COMMUNICATION.
 CC -1- SUBUNIT: MAY FORM HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
 CC LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
 CC MEMBRANES.
 CC -1- DISEASE: REDUCED CONCENTRATIONS OF MOG ARE OBSERVED IN JIMPY AND
 CC QUACKING DYSMYELINATING MUTANT MICE.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE V-LIKE DOMAIN. BELONGS TO THE B2M/MOG SUBFAMILY.
 CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)
 CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L29503; AAC42023.1; -;
 DR EMBL: L29498; AAC42023.1; JOINED.
 DR EMBL: L29500; AAC42023.1; JOINED.
 DR EMBL: L29501; AAC42023.1; JOINED.
 DR EMBL: L29499; AAC42023.1; JOINED.
 DR EMBL: L29502; AAC42023.1; JOINED.
 DR EMBL: U64572; AAB08096.1; -;
 DR EMBL: L20942; AAA03180.1; -;
 DR MGD: MGI:97435; MOG.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SMO0406; IgV_1.

KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 246
 FT DOMAIN 29 156 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
 FT TRANSMEM 157 177 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 178 209 POTENTIAL.
 FT TRANSMEM 210 230 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 231 246 POTENTIAL.
 FT DOMAIN 45 133 EXTRACELLULAR (POTENTIAL).
 FT DISULFD 52 126 IG-LIKE V-TYPE DOMAIN.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CONFLICT 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 32 32 L -> G (IN REF. 2).
 FT CONFLICT 95 95 R -> G (IN REF. 4).
 FT CONFLICT 169 169 G -> E (IN REF. 3).
 FT CONFLICT 169 169 P -> S (IN REF. 2).
 SO SEQUENCE 246 AA; 28271 MW; 1F7A84A0D5CFB89 CRC64;
 Query Match 9.6%; Score 150.5; DB 1; Length 246;
 Best Local Similarity 23.8%; Pred. No. 2.5e-05;
 Matches 34; Conservative 33; Mismatches 65; Indels 11; Gaps 2;
 QY 37 WS-----TISIIILAGALILIGFSGRHSITVTYVASAGNIGEDGILSCTEPEPIK 90
 DB 5 WFSWSPSCFLSLILL-----LQLSCSYAGQPRVIGPGYPIRALVGDEALELPCRSIPKN 59
 QY 91 LSDIYIOMKEVGLVHEFEKQDELSEODEMFGRVAFDQYIVGNASRLKNQOLT 150
 DB 60 AMGMEVGYRSPFSRVVHLHYRNGKDQDAQAEYRGRELAKETISEGVTLRIQNVRS 119
 QY 151 DAGTYKCYITTSKGNANLEYK 173
 DB 120 DEGGYTCFPRDHSYQEAAMELK 142
 RESULT 7
 ICOL_HUMAN
 ID ICOL_HUMAN STANDARD: PRT: 302 AA.
 AC 075144; Q9NR01; Q9HD18;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ICOS LIGAND PRECURSOR (B7 HOMOLOG 2) (B7-H2) (B7-LIKE PROTEIN GL50)
 DE (B7-RELATED PROTEIN-1) (B7RP-1).
 GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Dendritic cell;
 RX PubMed=11023515;
 RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
 RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds
 RT ICOS.";
 RL Blood 96:2808-2813(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC TISSUE=Peripheral blood lymphocytes;
 RX PubMed=11007762;
 RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
 RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han K.,
 RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Cocchia M.A.;
 RT "Characterization of a new human B7-related protein: B7RP-1 is the
 RT ligand to the co-stimulatory protein ICOS.";
 RL Int. Immunol. 12:1439-1447(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Leukocyte;
 RX MEDLINE=20126021; PubMed=10657606;
 RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
 RA Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,

RA Jacobs K.A., Collins M.;
 RT "Identification of GLS0, a novel B7-like protein that functionally
 RT binds to ICOS receptor.";
 RL J. Immunol. 164:1653-1657(2000).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 RN (5)
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Ling V., Dunussi-Joannopoulos K.;
 RT "G150 molecules and uses thereof.";
 RL Patent number WO0121796, 29-MAR-2001.
 CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: 1 (SHOWN HERE) AND 2;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
 CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
 CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUCOCYTES,
 CC SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN
 CC LYMPH NODES, LEUCOCYTES AND SPLEEN.
 CC -1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
 CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
 CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
 CC -1- SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. B7N/MOG
 CC SUBFAMILY.
 CC -1- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITION 300
 CC ONWARD FOR AN UNKNOWN REASON.
 CC -----
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF199028; AAF34739.1; -;
 DR EMBL: AF289028; AAG01176.1; -;
 DR EMBL: AF216749; AAK16241.1; -;
 DR EMBL: AB014553; BAA31628.1; ALT_SEQ.
 DR EMBL: AX100595; CAC36465.1; -;
 DR MIM: 605717; -;
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00409; Ig; 1.
 KW B-cell activation; Immune response; Glycoprotein;
 KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 KW Alternative splicing.
 FT SIGNAL 1 18
 FT CHAIN 19 302 POTENTIAL.
 FT DOMAIN 19 256 ICOS LIGAND.
 FT TRASMEM 257 277 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 278 302 POTENTIAL.
 FT DOMAIN 30 302 CTOPPLASMIC (POTENTIAL).
 FT DOMAIN 120 120 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 151 223 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 37 113 POTENTIAL.

FT DISULFID 158 216 POTENTIAL.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 300 302 GHV -> ESMNILLILS (IN ISOFORM 2).
 SO SEQUENCE 302 AA; 33349 MM; 647934E21B55E34A CRC64;
 Query Match 9.4%; Score 147.5; DB 1; Length 302;
 Best Local Similarity 24.5%; Pred. No. 5,9e-05;
 Matches 66; Conservative 41; Mismatches 117; Indels 45; Gaps 13;
 QY 75 IGEDGILSTCFEPD---IKISDIYIOMKGVGLVHEFREGDEISEODEMFRGRTAVF 131
 DB 29 VGSDELVELSCAC-DEGSRFDINDYVYQTSKSTVYTHIPQNSLLENVDSRYRNLALMS 87
 QY 132 ADVYVGNASRLKKNQVLTAGTYKCIITSRKG-----NANLEKRTGA-FSMPEYVND 185
 DB 88 PAGMLRKDFSLRLFNVTVPDEQKFC-LVLSQSLGFEVLVSVTLHVANFSPVVSAP 146
 QY 186 YNASE--TLRCEAPRWFPOPTVWASOVDOGANFSEVNTSPELNSENTMKVSVLYN 243
 DB 147 HSPQDELITFTCTISINCPRPYVWINKTNSLLDQALNDYVFLNMRGL-YDVSVYLRI 205
 QY 244 V-TINNTYSCMIEN-----DIAKATG-DI---KVTSEI---KRSHQLLNLSKAS 286
 DB 206 ARPTSVNIGCCINLVLLQQLTVGSQGTGNDIGERDKITPEVSTGEKNATWSILAVLCL 265
 QY 287 L-----CYSSFFALSMA LLP 301
 DB 266 LVVVAIVAGVCRDRCILQHSYAGAMAVSP 294
 RESULT 8
 ID CD86_HUMAN STANDARD; PRT; 329 AA.
 AC P42081; Q13655;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 20-AUG-2001 (Rel. 40, last annotation update)
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2
 DE ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.2) (B70) (FUN-1) (B063).
 GN CD86 OR CD28LGZ.
 OS Homo sapiens (Human).
 OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94053735; PubMed=7694363;
 RA Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,
 RA Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;
 RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
 RT cell proliferation.";
 RL Science 262:909-911(1993).
 RN [2]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX MEDLINE=94050123; PubMed=7694153;
 RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
 RA Lanier L.L., Somoza C.;
 RT "B70 antigen is a second ligand for CTLA-4 and CD28.";
 RL Nature 366:76-79(1993).
 RN [3]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX TISSUE=Forebrain;
 RC MEDLINE=95351831; PubMed=7541777;
 RA Jellis C.L., Wang S.S., Rennett P., Borriello F., Sharpe A.H.,
 RA Green N.R., Gray G.S.;
 RT "Genomic organization of the gene coding for the costimulatory human
 RT B-lymphocyte antigen B7-2 (CD86).";
 RL Immunogenetics 42:85-89(1995).

RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=95088403; PubMed=7527824;
 RA Lanier L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Azuma M.;
 RT "CD80 (B7) and CD86 (B7.1) provide similar costimulatory signals for T
 RT cell proliferation, cytokine production, and generation of CTL.";
 RL J. Immunol. 154:97-105(1995).
 RN [5]
 RP IDENTIFICATION AS CD86.
 RX MEDLINE=94348060; PubMed=7520767;
 RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,
 RA Nadler L.M., Makasa H., Tedder T.F.;
 RT "The B7-2 (B7.0) costimulatory molecule expressed by monocytes and
 RT activated B lymphocytes is the CD86 differentiation antigen.";
 RL Blood 84:1402-1407(1994).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS.
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
 CC MONOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -1- DATABASE: NAME-PROT; NOTE-CD guide CD86 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prot/cd/cd86.htm".
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 DR EMBL: L25259; AAB58389.1; -;
 DR EMBL: U04343; AAB03814.1; -;
 DR EMBL: U17722; AAB86473.1; -;
 DR EMBL: U17717; AAB86473.1; JOINED.
 DR EMBL: U17718; AAB86473.1; JOINED.
 DR EMBL: U17719; AAB86473.1; JOINED.
 DR EMBL: U17721; AAB86473.1; JOINED.
 DR MIM: 601020; -;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00290; IG_MHC; FALSE_NEG.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 329 T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
 FT DOMAIN 24 247 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 248 268 POTENTIAL.
 FT DOMAIN 269 329 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 149 225 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 40 110 POTENTIAL.
 FT DISULFID 157 218 POTENTIAL.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 27 27 K -> E (IN REF. 3).
 SQ SEQUENCE 329 AA; 37696 MW; 65DAF382689CFFD CRC64;

Query Match 9.4%; Score 147.5; DB 1; Length 329;
 Best Local Similarity 23.4%; Pred. No. 6,7e-05;
 Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;
 QY 50 IALIGFQISGRHSITVTYVASAGNIGEDGILCTF--EPDKISDIYIOMLKGVGLV 107
 DB 12 ILFWAFILLSGAAPLKIQA-----FNETADLPQFANSONQSLSELYFVQDGNL-VL 65
 QY 108 HEFKGDELSEQDEMERGRTAVFADVOYVGNASLRKLVNOLTAGYIKCIYITSKGK- 166
 DB 66 NEVLATGKEKFDVSHSKYKGRSFDS-----SWTLRLNLIQIKDKGLQCIHHRKPKGM 120
 QY 167 ---NANLEYTGA-FESMEY-----NDYNASSETLRCEAPRPPVTVVASQVDGAN 217
 DB 121 IRIHOMSELVLANFSQPEIYPIISNTEYIT-NLTCSSIHGIPR----- 166
 QY 218 FSEVNTSFELSENVTYKV-----VSLEYNTI-----NNTYSMIEN 256
 DB 167 ---KKMSVLLRTKNSITFEDYDGMQSDQNTELYDVISLSVGFDPVTSMTIFCILET 222
 QY 257 DIAKATGDKTESEIKR-RSHQLDLS---KSLCYSSFFAISW 297
 DB 223 DKTRLSSPFSIELEDPPQPPDHPITVAVLPVYIICVWFCLILW 268
 RESULT 9
 CD86_RABIT STANDARD; PRT; 330 AA.
 ID CD86_RABIT
 AC P42071;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2
 DE ANTIGEN).
 GN CD86.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHB:HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules".
 RL Immunogenetics 42:217-220(1995).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: D49842; BAA08642.1; -;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 22 POTENTIAL.

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FT CHAIN 23 330 B LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT DOMAIN 23 247 POTENTIAL.
FT TRANSMEM 248 268 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 269 330 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 333 117 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 149 225 POTENTIAL.
FT DISULFID 40 110 POTENTIAL.
FT CARBOHYD 157 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 330 AA: 37142 MW: 935CD65C57E3EB1 CRC64:

Query Match 9.4%; Score 147.5; DB 1; Length 330;
Best Local Similarity 24.0%; Pred. No. 6.7e-05;
Matches 59; Conservative 44; Mismatches 80; Indels 63; Gaps 11;

QY 38 SIISITITAGATATITGFGISGRHSITVTVASAGNIGEDGILCTF--EPDIKLSDIY 95
DB 12 TVEFMALLLSGASLRI-----QAYFNKTADLPQFTMSQSRSISELY 54
QY 96 IOWLKEGVGLVHEFEKGEDELSEODEMFRGAVADQYVGNASIRKLVOLTADGY 155
DB 55 VEFQDERL-VLELFLGRKKPDNPVKYIGRTSF--DQ---ESMWLOLNVOIKKGY 108
QY 156 KCIYITSKGK-----NANLEYTGA-FSMPEYVNDYNA---SSETLRCEAPWPPQPV 206
DB 109 QCVHHRGAKGLPIYOMSELVLANFOPETLITNSRNAINLTSSVQGYDEPK 168
QY 207 VNASQVDGANESEVNTSEFELSENVTMKV-----VSILYVNTINNTSCMIEN 256
DB 169 MF-----FVLKTENATTEYDGVIEKSDQNTVGLYNISISG--STFSD 209
QY 257 DIAKAT 262
DB 210 DIRNAT 215

RESULT 10
MOG_HUMAN STANDARD: PRT: 247 AA.
AC Q16653: Q14855: Q13054: Q13055: Q92891: Q92892: Q92893: Q92894;
AC Q92895: Q93053: Q99605: Q00713: Q00714: Q00715;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
GN MOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE-95310943: PubMed-7790876;
RA Hilton A.A., Slavin A.J., Hilton D.J., Bernard C.C.A.;
RT "Characterization of cDNA and genomic clones encoding human myelin
RT oligodendrocyte glycoprotein."
RL J. Neurochem. 65:309-318(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-95054056: PubMed-7964757;
RA Pham-Dinh D., Allingant B., Ruberg M., della Gaspera B.,
RA Nussbaum J.-L., Dautigny A.;
RT "Characterization and expression of the cDNA coding for the human
RT myelin/oligodendrocyte glycoprotein."

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RL J. Neurochem. 63:2353-2356(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-96015053: PubMed-8530032;
RA Roth M.-P., Malfroy L., Offer C., Sevin J., Enault G., Borot N.,
RA Pontarotti P., Coppin H.;
RT "The human myelin oligodendrocyte glycoprotein (MOG) gene: complete
RT nucleotide sequence and structural characterization."
RL Genomics 28:241-250(1995).
RN [4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE-96115584: PubMed-8666381;
RA Pham-Dinh D., della Gaspera B., de Rosbo N.K., Dautigny A.;
RT "Structure of the human myelin/oligodendrocyte glycoprotein gene and
RT multiple alternative spliced isoforms."
RL Genomics 29:345-352(1995).
RN [5]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RA Ballenthin P.A., Gardiner M.V.;
RL Submitted (Sep-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP STRUCTURE BY NMR OF 64-84.
RX MEDLINE-97354172: PubMed-9210466;
RA Albouze-Abo S., Wilson J.C., Bernard C.C.A., von Itzstein M.;
RT "A conformational study of the human and rat encephalitogenic myelin
RT oligodendrocyte glycoprotein peptides 35-55."
RL Eur. J. Biochem. 246:59-70(1997).
CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
CC COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
CC CELL COMMUNICATION.
CC -1- SUBUNIT: MAY FORM HOMO- OR HETERODIMERS BETWEEN THE DIFFERENT
CC ISOFORMS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (ISOFORMS ALPHA-1
CC AND BETA-1); TYPE I MEMBRANE PROTEIN (OTHER ISOFORMS) (POTENTIAL).
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 9 ISOFORMS: ALPHA-1 (SHOWN HERE),
CC -2, -3, -4, BETA-1, -2, -3, -4 AND A SHORT ISOFORM ARE PRODUCED BY
CC ALTERNATIVE SPLICING. THE SHORT ISOFORM IS NOT FUNCTIONALLY
CC ACTIVE. IT MAY BE EXPRESSED AT LOW LEVEL IN THE ADULT.
CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
CC LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
CC MEMBRANES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE DOMAIN. BELONGS TO THE RTN/MOG SUPERFAMILY.
CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)
CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X74511: CAA52617.1; -
DR EMBL: Z48051: CAA88109.1; -
DR EMBL: U18840: AAC50361.1; -
DR EMBL: U18843: AAC50362.1; -
DR EMBL: U18798: AAC50876.1; -
DR EMBL: U18799: AAC50877.1; -
DR EMBL: U18800: AAB36870.1; -
DR EMBL: U18801: AAC50878.1; -
DR EMBL: U18803: AAC50879.1; -
DR EMBL: U64564: AAB08088.1; -
DR EMBL: U64565: AAB08089.1; -
DR EMBL: U64566: AAB08090.1; -
DR EMBL: U64567: AAB08091.1; -
DR EMBL: U64568: AAB08092.1; -
DR EMBL: U64569: AAB08093.1; -
DR EMBL: U64570: AAB08094.1; -
DR EMBL: U64571: AAB08095.1; -
DR HSSP: O13740: 1KTC.
MIM: 159465; -.

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DR	InterPro: IPRO03006; Ig_MHC.
KW	Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal;
FT	Signal
FT CHAIN	1 29 POTENTIAL.
FT DOMAIN	30 247 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
FT TRANSMEM	30 154 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	155 175 POTENTIAL.
FT DOMAIN	176 210 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	211 231 POTENTIAL.
FT DOMAIN	232 247 EXTRACELLULAR (POTENTIAL).
FT DOMAIN	46 134 IG-LIKE V-TYPE DOMAIN.
FT DISULFID	53 127 POTENTIAL.
FT CARBOHYD	60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC	30 145 MISSING (IN ISOFORM ALPHA-4).
FT VARSPPLIC	198 203 DPHFR -> GREYHV (IN SHORT ISOFORM).
FT VARSPPLIC	204 247 MISSING (IN SHORT ISOFORM).
FT VARSPPLIC	198 236 DPHFRPKCKITLIVTAVPAVGLPALVIICMYMLHRRRLA -> ESFEVLGQVEKPEPT (IN ISOFORM ALPHA-3 AND ISOFORM BETA-3).
FT FT	MISSING (IN ISOFORM ALPHA-2 AND ISOFORM BETA-2).
FT VARSPPLIC	198 236 MISSING (IN ISOFORM BETA-4).
FT VARSPPLIC	198 243 RNPF -> LFFLEALSG (IN ISOFORM BETA-1, ISOFORM BETA-2, ISOFORM BETA-3 AND ISOFORM BETA-4).
FT FT	V -> L (IN REF. 3).
FT CONFLICT	171 171
SO SEQUENCE	247 AA; 28179 MW; 847601FE597AB0C CRC64;

Query Match	9.1%	Score 144;	DB 1;	Length 247;
Best Local Similarity	20.8%	Pred. 8.7e-05;		
Matches 49;	Conservative 39;	Mismatches 80;	Indels 68;	Gaps 6

[illegible]

RESULT	11			
CD86_MOUSE				
ID	CD86_MOUSE	STANDARD;	PRT;	309 AA.
AC	P42082;			
DT	01-NOV-1995	(Rel. 32, Created)		
DT	01-NOV-1995	(Rel. 32, Last sequence update)		
DT	20-AUG-2001	(Rel. 40, Last annotation update)		
DE	T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2			
GN	ANTIGEN) (EARLY T CELL COSTIMULATORY MOLECULE-1) (ETC-1).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumeleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclerognathii; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94065585; Pubmed=7504059;			
RA	Freeman G.J., Borriello F., Hodes R.J., Reiser H., Gribben J.G.,			
RA	Ng J.W., Kim J., Goldberg J.M., Hattcock K., Laszlo G., Lombard L.A.,			
RA	Wang S., Gray G.S., Nadler L.M., Sharpe A.H.,			
RT	"Murine B7-2, an alternative CD14 counter-receptor that costimulates			
RT	T cell proliferation and interleukin 2 production."			

RL	J.	Exp.Med.	178:	2185-2192(1993).
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-129;			
RX	MEDLINE=96094437; PubMed=7499829;			
RA	Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;			
RT	"differential expression of alternate MB7-2 transcripts.";			
RL	J. Immunol.	155:	5490-5497(1995).	
RN	[3]			
RP	SEQUENCE OF 7-309 FROM N.A.			
RX	MEDLINE=94230971; PubMed=7513726;			
RA	Chen C., Gault A., Shen L., Nabavi N.;			
RT	"Molecular cloning and expression of early T cell costimulatory molecule-1 and its characterization as B7-2 molecule.";			
RL	J. Immunol.	152:	4929-4936(1994).	
CC	-1-	FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.		
CC	-1-	SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	-1-	TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.		
CC	-1-	SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.		
CC	-1-	CUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.		
CC		THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/or send an email to license@isb-sib.ch).		
DR	EMBL	L25606	AAA97770.1	-
DR	EMBL	U39456	AAC52334.1	-
DR	EMBL	U39459	AAC52334.1	JOINED.
DR	EMBL	U39461	AAC52334.1	JOINED.
DR	EMBL	U39462	AAC52334.1	JOINED.
DR	EMBL	U39463	AAC52334.1	JOINED.
DR	EMBL	U39464	AAC52334.1	JOINED.
DR	EMBL	U39465	AAC52334.1	JOINED.
DR	EMBL	U39456	AAC52336.1	ALY_INT.
DR	EMBL	U39461	AAC52336.1	JOINED.
DR	EMBL	U39462	AAC52336.1	JOINED.
DR	EMBL	U39463	AAC52336.1	JOINED.
DR	EMBL	U39464	AAC52336.1	JOINED.
DR	EMBL	U39465	AAC52336.1	JOINED.
DR	EMBL	U39466	AAC52336.1	JOINED.
DR	EMBL	U39467	AAB30744.2	ALT_INT.
DR	MDG	MGI:101773	CDB6	
DR	InterPro	IPR003006	Ig_MHC	
DR	InterPro	IPR003596	Ig_V	
DR	SMART	SMO0406	IGV_1	
DR	PROSITE	PS00290	IG_MHC	FALSE NEG.
KW	Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane; Receptor.			
FT	SIGNAL	1	23	POTENTIAL.
FT	CHAIN	24	309	T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT	DOMAIN	24	244	EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	245	265	POTENTIAL.
FT	DOMAIN	266	309	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	33	117	IG-LIKE V-TYPE DOMAIN.
FT	DOMAIN	149	223	IG-LIKE C2-TYPE DOMAIN.
FT	DISULEID	40	110	POTENTIAL.
FT	CARBOHYD	157	216	POTENTIAL.
FT	CARBOHYD	33	33	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	47	47	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	92	92	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	146	146	N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 309 AA; 34665 MW; 8F58DCD1F81D5EA CRC64;

Query Match
Best Local Similarity 22.6%; Score 143.5; DB 1; Length 309;
Matches 50; Conservative 53; Mismatches 83; Indels 35; Gaps 10;

OY 64 ITVTVAASAGNT-----GEGDILSTCF--EPDIKLSDIVIOMLKEGVGLVHEFEKGD 115
DB 15 VVLLISDADVSVETQAVFNCTAYLPCEFTKAGNISSELVFVWQDQKL-VLEYHLGTE 73
OY 116 ELSEODEMFRGRTAVFADQVIVGNASLRKLVQTLTLAGTYKCIITTSKGNANLEK-- 173
DB 74 KLDVNAKILGRTSF--DR---NNWTLRLHNVQIKDMGSDYDCKIQKPPGSIILQDTLL 128
OY 174 ---TGAFSPMEVNVVDYVNASSET---LRCEAPRMPPOPVYVNASQVQDQANFSEVSNTSF 226
DB 129 ELSTVIANFSEPEIKLQNTNGSINGILTCTSKGHRKPKMIFLITNSTNETGD----NM 184
OY 227 ELNSEVNTKVVSVLYNVTI-----NNTYSCEMIENDIAK 260
DB 185 QISQDNVT-ELFSISNSLSLSPDPGVHMTVVCVLETESMK 224

RESULT 12
MOG_BOVIN
ID MOG_BOVIN STANDARD; PRT; 246 AA.
AC P55803;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
GN MOG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 63-70.
RC TISSUE=Brain;
RX MEDLINE=93376728; PubMed=8367453;
RA Pham-Dinh D., Mattei M.G., Nussbaum J.-L., Roussel G.,
RA Pontarotti P., Roedel N., Mather I.H., Artzt K., Lindahl K.F.,
RA Daultigny A.;
RT "Myelin/oligodendrocyte glycoprotein is a member of a subset of the
RT immunoglobulin superfamily encoded within the major
RT histocompatibility complex.";
RL proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
RN [2]
RP SEQUENCE OF 29-36.
RC TISSUE=Brain;
RX MEDLINE=93382604; PubMed=8371836;
RA Birling M.C., Roussel G., Nussbaum F., Nussbaum J.-L.;
RT "Biochemical and immunohistochemical studies with specific polyclonal
RT antibodies directed against bovine myelin/oligodendrocyte
RT glycoprotein.";
RL Neurochem. Res. 18:937-945(1993).
CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
CC COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
CC CELL COMMUNICATION.
CC -1- SUBUNIT: MAY FORM HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
CC LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
CC MEMBRANES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE DOMAIN. BELONGS TO THE B2M/MOG SUBFAMILY.
CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)

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CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
CC -----
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CC -----
DR EMBL: L21757; NOT_ANNOTATED_CDS.
DR HSSP: Q13740; KJC.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
FT SIGNAL 1 28
FT CHAIN 1 28
FT DOMAIN 29 246 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
FT TRANSMEM 154 174 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 175 209 POTENTIAL.
FT TRANSMEM 210 230 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 231 246 POTENTIAL.
FT DOMAIN 45 133 EXTRACELLULAR (POTENTIAL).
FT DISULFID 52 126 IC-LIKE V-TYPE DOMAIN.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 246 AA; 28028 MW; 363C76AB1A33DE41 CRC64;

Query Match
Best Local Similarity 26.1%; Score 140.5; DB 1; Length 246;
Matches 31; Conservative 25; Mismatches 50; Indels 13; Gaps 1;

OY 68 TVASAGN-----IGEDGILSTCFEPDIKLSDIVIOMLKEGVGLVHEFEKGD 114
DB 24 TSSSAGQFNVIGRPHIRALVGDVDELLPCRISPGKATGMEGVYRPPSRVYHLRNCK 83
OY 115 DELSEODEMFRGRTAVFADQVIVGNASLRKLVQTLTLAGTYKCIITTSKGNANLEK 173
DB 84 DODEGAPRYRGRTOLEKETIGEGKVTLRIRNVRFSDGFCFFRDSYGEAAMELK 142

RESULT 13
NCA2_HUMAN
ID NCA2_HUMAN STANDARD; PRT; 761 AA.
AC P13592; P13593;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NEURAL CELL ADHESION MOLECULE, PHOSPHATIDYLINOSITOL-LINKED ISOFORM
DE PRECURSOR (N-CAM 120) (NCAM-120) (CD56 ANTIGEN).
GN NCAM1 OR NCAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (N-CAM 120).
RC TISSUE=Skeletal muscle;
RX MEDLINE=89305258; PubMed=3253057;
RA Barton C.H., Dickson G., Gower H.J., Rowett L.H., Putt W.,
RA Elsom V., Moore S.E., Goridis C., Walsh F.S.;
RT "Complete sequence and in vitro expression of a tissue-specific
RT phosphatidylinositol-linked N-CAM isoform from skeletal muscle.";
RL Development 104:165-173(1988).
RN [2]
RP SEQUENCE OF 491-761 FROM N.A. (N-CAM 120).
RC TISSUE=Skeletal muscle;
RX MEDLINE=87301755; PubMed=2887295;
RA Dickson G., Gower H.J., Barton C.H., Prentice H.M., Elsom V.L.,
RA Moore S.E., Cox R.D., Quinn C., Putt W., Walsh F.S.;
RT "Human muscle neural cell adhesion molecule (N-CAM): identification

```

RT of a muscle-specific sequence in the extracellular domain."
 RL Cell 50:1119-1130(1987).
 RN [3]
 RP SEQUENCE OF 491-655 FROM N.A. (SECRETED ISOFORM).
 RX MEDLINE=90077532; PubMed=3203385;
 RA Gower H.J., Barton C.H., Elsom V.L., Thompson J., Moore S.E.,
 RA Dickson G., Walsh F.S.;
 RT "Alternative splicing generates a secreted form of N-CAM in muscle
 and brain".
 RT Cell 55:955-964(1988).
 CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
 CC NEURITES, ETC.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
 CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD56 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd56.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X16841; CAA34739.1; -
 CC EMBL: M17409; AAA59912.1; -
 CC EMBL: M22094; AAA59910.1; -
 CC EMBL: M22092; AAA59911.1; -
 CC EMBL: M22091; AAA59911.1; JOINED.
 CC PIR: S07784; IJHUNG.
 CC PIR: A31635; A31635.
 CC MIM: 116930; -
 CC InterPro: IPR001777; FN.III.
 CC InterPro: IPR003006; IG.MHC.
 CC InterPro: IPR003598; IG.C2.
 CC Pfam: PF00041; fn3; 2.
 CC Pfam: PF00047; Ig; 5.
 CC SMART: SM00060; FN3; 2.
 CC SMART: SM00408; IGc2; 5.
 CC KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Repeat; Signal;
 CC GPI-anchor; Alternative splicing.
 CC FT SIGNAL 1 19
 CC CHAIN 20 761
 CC FT
 CC DOMAIN 34 103 NEURAL CELL ADHESION MOLECULE,
 CC FT DOMAIN 132 196 PHOSPHATIDYLINOSITOL-LINKED ISOFORM.
 CC FT DOMAIN 228 294 IG-LIKE C2-TYPE DOMAIN 1.
 CC FT DOMAIN 322 392 IG-LIKE C2-TYPE DOMAIN 2.
 CC FT DOMAIN 419 486 IG-LIKE C2-TYPE DOMAIN 3.
 CC FT DOMAIN 518 595 IG-LIKE C2-TYPE DOMAIN 4.
 CC FT DOMAIN 660 727 FIBRONECTIN TYPE-III 1.
 CC FT DISULFID 41 96 FIBRONECTIN TYPE-III 2.
 CC FT DISULFID 139 189 PROBABLE.
 CC FT DISULFID 235 287 PROBABLE.
 CC FT DISULFID 329 385 PROBABLE.
 CC FT DISULFID 426 479 PROBABLE.
 CC FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 449 449 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPLIC 635 655 GEPSAPLECGMGEDGNSIV -> NIAOHCCNMFGAGLH
 CC FT NALMK (IN SECRETED ISOFORM).
 CC FT SEQUENCE 761 AA: 83770 MW: F0CAD3292D7AB67E CRC64; .

Query Match

8.6%; Score 135; DB 1; Length 761;

Best Local Similarity 23.2%; Pred. No. 0.0022;
 Matches 64; Conservative 49; Mismatches 11; Indels 52; Gaps 13;
 QY 63 SITVTVASAGNIGEDGILSTF-----EPDIKLSIVIQWLKEGYLGVHEKEGDE 116
 Db 77 SSSYTLTIA-NIDDAIGYKCVGVGEDGSESEATVNFQKLFKNAPPPQEFREGEDA 135
 QY 117 LSEDDEN-----FRGTAVFAQV---YGNASLRKNVQLDAGYKCYIITSK 163
 Db 136 VIVCDVVSLEPTTIKHKKGVDYLRKDVREIVTSNNYLOIGIKTKDEGYRC-----E 190
 QY 164 G-----KSNANLEYTKGAFSPE-----VNVVDN-ASSETLRCAPRPFQPTVWAS 210
 Db 191 GRILAREINKDQIVYVNPPTIQANQIVNATNANLGQSTVLCDA-EGPPEPTMGWK 249
 QY 211 QVDGAGNFSEVSNFSFELSENVTMKVSVLYNVTINNTYSCTMIENDIAK--ATGDIKVT 268
 Db 250 DGEIQEEDDEDEKTFSDSSQTLIKRV---DKNDEAEYICIAENKAGEDATIHKVF 305
 QY 269 E-----SEIKRSHQLNKSASLCVSS---FFAISW 297
 Db 306 AKPRITVYENQTALEBQYTLTCEASGDPIPSITW 341
 RESULT 14
 NCAL_HUMAN STANDARD; PRT; 848 AA.
 AC P13591; Q16180; Q15829;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NEURAL CELL ADHESION MOLECULE, 140 KDA ISOFORM PRECURSOR (N-CAM 140)
 DE (NCAM-140) (CD56 ANTIGEN).
 GN NCAM1 OR NCAM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94356433; PubMed=80759973;
 RA Saito S., Tani Y., Tachibana I., Hayashi S., Kishimoto T., Kawase I.;
 RT "Complementary DNA sequence encoding the major neural cell adhesion
 RT molecule isoform in a human small cell lung cancer cell line.";
 RL Lung Cancer 10:307-318(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91250739; PubMed=1710251;
 RA Lanier L.L., Chang C., Azuma M., Rutenberg J.J., Hemperly J.J.,
 RA Phillips J.H.;
 RT "Molecular and functional analysis of human natural killer cell-
 RT associated neural cell adhesion molecule (N-CAM/CD56)."
 RL J. Immunol. 146:4421-4426(1991).
 RN [3]
 RP SEQUENCE OF 491-848 FROM N.A.
 RX MEDLINE=87301755; PubMed=2887295;
 RA Dickson G., Gower H.J., Barton C.H., Prentice H.M., Elsom V.L.,
 RA Moore S.E., Cox R.D., Quinn C., Putt W., Walsh F.S.;
 RT "Human muscle neural cell adhesion molecule (N-CAM): identification
 RT of a muscle-specific sequence in the extracellular domain".
 RL Cell 50:1119-1130(1987).
 CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
 CC NEURITES, ETC.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
 CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD56 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd56.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL: S71824; AAB31836.1; -
 DR EMBL: U63041; AAB04558.1; -
 DR EMBL: M17410; AAA59913.1; -
 DR PIR: B26883; B26883.
 DR MIM: 116930; -
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003598; IG_C2.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00408; IGc2; 5.
 DR Immunoglobulin domain; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 848
 FT DOMAIN 20 708
 FT TRANSMEM 709 729
 FT DOMAIN 730 848
 FT DOMAIN 34 103
 FT DOMAIN 132 196
 FT DOMAIN 228 294
 FT DOMAIN 322 392
 FT DOMAIN 419 486
 FT DOMAIN 518 595
 FT DOMAIN 660 727
 FT DISULFID 41 96
 FT DISULFID 139 189
 FT DISULFID 235 287
 FT DISULFID 329 385
 FT DISULFID 422 479
 FT CARBOHYD 222 222
 FT CARBOHYD 315 315
 FT CARBOHYD 347 347
 FT CARBOHYD 423 423
 FT CARBOHYD 449 449
 FT CARBOHYD 478 478
 FT CONFLICT 215 215
 FT CONFLICT 239 239
 FT CONFLICT 490 490
 FT CONFLICT 599 600
 FT CONFLICT 720 721
 FT CONFLICT 811 811
 SO SEQUENCE 848 AA; 93360 MW; 68D2F0C0E6C1C2AD CRC64;

Query Match 8.6%; Score 135; DB 1; Length 848;
 Best Local Similarity 23.2%; Pred. No. 0.0026;
 Matches 64; Conservative 49; Mismatches 111; Indels 52; Gaps 13;

QY 63 SITVTASAGNIGEDGLSTF-----EPDIKSDIYIOWLEGLVGLVHEKRGDE 116
 DB 77 SSSLTITLYNA-NIDAGIYKCVTGEDSESEATVNVKIFQKLMFNKAPFOEPFREGDA 135
 QY 117 LSEODEM-----FRGRTAVFADY---IYGNASLRKANKQVLDAGIYKCIITTSK 163
 DB 136 VIVCDVVSLLPPTIIWKHKGDVILIKKDVRIIVSNNTLQIRGIKKKDEGTYRC-----E 190
 QY 164 G-----KGNANLEYKTGAEMPE-----VNVDPN-ASSETLCEAPRMFPPTVYVAS 210
 DB 191 GRIIARGEINFKDIQVIVNPTIOAQNINVMANALQGVTLVQDA-EGPEPEPTMSWTK 249
 QY 211 QVDOGANFSEVSNFSFELSENVTMKVSVLYNVTINNTYSCTMIENDIAK--ATGDIKVT 268
 DB 250 DGEIOEEDDEKRYIFSDSSQLTIKKV---DKNDEAYICIAENKAGDEDAIHLKVF 305

QY 269 E-----SEIKRRSHLQILNKSASICVSS---FPAISW 297
 DB 306 AKRKITYVENQTMLEDEQVTLTCEASGDPISITW 341

RESULT 15
 NCAL_BOVIN STANDARD: PRT: 853 AA.
 ID NCAL_BOVIN
 AC P31836;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NEURAL CELL ADHESION MOLECULE, 140 KDA ISOFORM PRECURSOR (N-CAM 140)
 DE (NCAM-140).
 GN NCAM1 OR NCAM.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain cortex;
 RX MEDLINE=89378239; PubMed=2776887;
 RA Lipkin V.M., Khramtsov N.V., Andreeva S.G., Moshnyakov M.V.,
 RA Petukhova G.V., Rakitina T.V., Feshchenko E.A., Ishchenko K.A.,
 RA Mirzoeva S.F., Chernova M.N., Dranyatsyna S.M.;
 RT "Calmodulin-independent bovine brain adenylyl cyclase. Amino acid
 RT sequence and nucleotide sequence of the corresponding cDNA.";
 RL FEBS Lett. 254:69-73(1989).
 RN [2]
 RP SEQUENCE OF 20-36.
 RX MEDLINE=86140120; PubMed=3512556;
 RA Rougon G., Marshak D.R.;
 RT "Structural and immunological characterization of the amino-terminal
 RT domain of mammalian neural cell adhesion molecules.";
 RL J. Biol. Chem. 261:3396-3401(1986).
 RN [3]
 RP IDENTIFICATION AS N-CAM.
 RX MEDLINE=92111748; PubMed=1765159;
 RA Premont R.T.;
 RT "A bovine brain cDNA purported to encode calmodulin-insensitive
 RT adenylyl cyclase has extensive identity with neural cell adhesion
 RT molecules (N-CAMs).";
 RL FEBS Lett. 295:230-231(1991).
 CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
 CC NEURITES, ETC.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
 CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A CALMODULIN-
 CC INDEPENDENT ADENYLYL CYCLASE.

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DR EMBL: X16451; CA34470.1; -
 DR PIR: A32976; IBOINC.
 DR HSP: P40189; IBOU.
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003598; IG_C2.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 5.

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